

94073

STIC-Biotech/ChemLib

From: Schultz, James
 Sent: Thursday, May 15, 2003 7:52 AM
 To: STIC-Biotech/ChemLib
 Subject: Seq Search 09/780,929

RECEIVED

MAY 15 2003

Hello,
 Could you please run a length limited nucleotide sequence search on SEQ ID NOS: 97 (15 nt long) and 98 (18 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 20 nucleotides long?
 Thanks,
 Doug Schultz

STIC-BIOTECH/CHEMLIB
(STIC)

STIC-Biotech/ChemLib

From: Schultz, James
 Sent: Thursday, May 15, 2003 7:53 AM
 To: STIC-Biotech/ChemLib
 Subject: But wait there's more--Seq Search 09/780,929

RECEIVED

MAY 15 2003

STIC-BIOTECH/CHEMLIB
(STIC)

The sequence search request below was just submitted--I forgot to include that I also need the interference databases searched. Thanks,
 Doug Schultz

-----Original Message-----

From: Schultz, James
 Sent: Thursday, May 15, 2003 7:52 AM
 To: STIC-Biotech/ChemLib
 Subject: Seq Search 09/780,929

Hello,
 Could you please run a length limited nucleotide sequence search on SEQ ID NOS: 97 (15 nt long) and 98 (18 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 20 nucleotides long?
 Thanks,
 Doug Schultz

TYPE OF SEARCH:

Searcher: _____
 Phone: _____
 Location: _____
 Date Picked Up: 5/16
 Date Completed: 5/25
 Searcher Prep/Review: _____
 Clerical: _____
 Online time: _____

NA Sequences: _____
 AA Sequences: _____
 Structures: _____
 Bibliographic: _____
 Litigation: _____
 Full text: _____
 Patent Family: _____
 Other: _____

VENDOR/COST (where applic.)

STN: _____
 DIALOG: _____
 Questel/Orbit: _____
 DRLink: _____
 Lexis/Nexis: _____
 Sequence Sys.: _____
 WWW/Internet: _____
 Other (specify): _____

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 16:53:27 ; Search time 871.364 Seconds

(Without alignments)
500.987 Million cell updates/sec

Title: us-09-780-929-97

Perfect score: 15

Sequence: 1 aguaacgugaagau 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 332216

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_pa:*

2: gb_hlg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hlg_hum:*

31: em_hlg_iny:*

32: em_hlg_other:*

33: em_hlg_mus:*

34: em_hlg_pln:*

35: em_hlg_rod:*

36: em_hlg_mam:*

37: em_hlg_vtl:*

38: em_sy:*

39: em_hlgo_hum:*

40: em_hlgo_mus:*

41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	15	100.0	15	6	AX214295	AX214295 Sequence
2	12	80.0	17	6	AX325565	AX325565 Sequence
3	12	80.0	17	6	AX325566	AX325566 Sequence
4	11	73.3	20	6	AX254729	AX254729 Sequence
5	11	73.3	20	6	AX255079	AX255079 Sequence
6	10.8	72.0	20	6	AX296064	AX296064 Sequence
7	10.8	72.0	20	6	AX304787	AX304787 Sequence
8	10.4	69.3	16	6	AX349237	AX349237 Sequence
9	10.4	69.3	17	6	AX272471	AX272471 Sequence
10	10.4	69.3	17	6	AX272472	AX272472 Sequence
11	10.4	69.3	17	6	AX272653	AX272653 Sequence
12	10.4	69.3	17	6	AX272654	AX272654 Sequence
13	10.4	69.3	17	6	AX272993	AX272993 Sequence
14	10.4	69.3	17	6	AX299883	AX299883 Sequence
15	10.4	69.3	17	6	AX325561	AX325561 Sequence
16	10.4	69.3	17	6	AX325562	AX325562 Sequence
17	10.2	68.0	15	6	AR033681	AR033681 Sequence
18	10.2	68.0	15	6	AR113503	AR113503 Sequence
19	10.2	68.0	15	6	I57910	I57910 Sequence 44
20	10.2	68.0	19	6	AR038557	AR038557 Sequence
21	10	66.7	16	6	A89154	A89154 Sequence 13
22	10	66.7	17	6	AX272473	AX272473 Sequence
23	10	66.7	18	6	AX110432	AX110432 Sequence
24	10	66.7	20	6	AX020035	AX020035 Sequence
25	10	66.7	20	6	AX295533	AX295533 Sequence
26	9.8	65.3	14	6	A15614	A15614 Oligonucleo
27	9.8	65.3	14	6	I04009	I04009 Sequence 5
28	9.8	65.3	15	6	AX008488	AX008488 Sequence
29	9.8	65.3	17	6	AR040477	AR040477 Sequence
30	9.8	65.3	17	6	AX227367	AX227367 Sequence
31	9.8	65.3	17	6	AX227387	AX227387 Sequence
32	9.8	65.3	18	6	A02405	A02405 Oligonucleo
33	9.8	65.3	18	6	AR106822	AR106822 Sequence
34	9.8	65.3	18	6	E32049	E32049 Antisense O
35	9.8	65.3	19	6	AX131036	AX131036 Sequence
36	9.8	65.3	19	6	AX131037	AX131037 Sequence
37	9.8	65.3	20	6	AR206662	AR206662 Sequence
38	9.8	65.3	20	6	AX148986	AX148986 Sequence
39	9.8	65.3	20	6	AX462586	AX462586 Sequence
40	9.6	64.0	17	6	AR162930	AR162930 Sequence
41	9.6	64.0	17	6	AR167259	AR167259 Sequence
42	9.6	64.0	17	6	AR206920	AR206920 Sequence
43	9.6	64.0	17	6	I33759	I33759 Sequence 5
44	9.6	64.0	17	6	I36972	I36972 Sequence 5
45	9.4	62.7	15	6	AR132924	AR132924 Sequence

ALIGNMENTS

RESULT 1

AX214295

LOCUS AX214295

DEFINITION Sequence 108 from Patent WO0159102.

ACCESSION AX214295

VERSION AX214295.1 GI:15524372

KEYWORDS

SOURCE

ORGANISM

synthetic construct.

artificial sequences.

REFERENCE

1 (bases 1 to 15)

AUTHORS Breaker, R. and Emliss, G.

TITLE Nucleozymes with endonuclease activity

JOURNAL Patent: WO 0159102-A 108 16-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)

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FEATURES
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    Location/Qualifiers
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        /db_xref="taxon:32630"
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Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      1 AGAUAACGUGAAGAU 15
Db      1 AGATAACGTGAAGAT 15
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RESULT 2
AX325565
LOCUS      AX325565      17 bp      DNA      linear      PAT 07-JAN-2002
DEFINITION Sequence 1703 from Patent WO0192512.
ACCESSION AX325565
VERSION    AX325565.1 GI:18096322
KEYWORDS
SOURCE
  ORGANISM
    Beta vulgaris.
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Caryophyllales; Chenopodiaceae; Beta.
REFERENCE
  AUTHORS      Kniec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
  TITLE        Targeted chromosomal genomic alterations in plants using modified
  JOURNAL      Patent: WO 0192512-A 1703 06-DEC-2001;
  ORGANISM     UNIVERSITY OF DELAWARE (US)
  LOCATION/Qualifiers
    1. 17
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      /db_xref="taxon:161934"
BASE COUNT      6 a      1 c      5 g      5 t
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Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      1 AGUAACGUGAA 12
Db      4 AGATAACGTGAA 15
|||||:|||||:

RESULT 3
AX325566/c
LOCUS      AX325566      17 bp      DNA      linear      PAT 07-JAN-2002
DEFINITION Sequence 1704 from Patent WO0192512.
ACCESSION AX325566
VERSION    AX325566.1 GI:18096323
KEYWORDS
SOURCE
  ORGANISM
    Beta vulgaris.
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Caryophyllales; Caryophyllales; Chenopodiaceae; Beta.
REFERENCE
  AUTHORS      Kniec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
  TITLE        Targeted chromosomal genomic alterations in plants using modified
  JOURNAL      Patent: WO 0192512-A 1704 06-DEC-2001;
  ORGANISM     UNIVERSITY OF DELAWARE (US)
  LOCATION/Qualifiers
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      /db_xref="taxon:161934"
BASE COUNT
ORIGIN

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BASE COUNT      5 a      5 c      1 g      6 t
ORIGIN

Query Match
Best Local Similarity 80.0%; Score 12; DB 6; Length 17;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      1 AGAUAACGUGAA 12
Db      14 AGATAACGTGAA 3
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RESULT 4
AX254729/c
LOCUS      AX254729      20 bp      DNA      linear      PAT 10-OCT-2001
DEFINITION Sequence 18 from Patent WO0171027.
ACCESSION AX254729
VERSION    AX254729.1 GI:16074396
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct.
    artificial sequences.
REFERENCE
  AUTHORS      Zohlhofer, D., Brauerle, P., Klein, C. and Neumann, F.J.
  TITLE        Mrna amplification
  JOURNAL      Patent: WO 0171027-A 18 27-SEP-2001;
  ORGANISM     Micromet AG (DE)
  LOCATION/Qualifiers
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BASE COUNT      4 a      6 c      5 g      5 t
ORIGIN

Query Match
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Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      5 AACGUGAAGAU 15
Db      13 AACGTGAAGAT 3
|||||:|||||:

RESULT 5
AX255079/c
LOCUS      AX255079      20 bp      DNA      linear      PAT 10-OCT-2001
DEFINITION Sequence 18 from Patent WO0170953.
ACCESSION AX255079
VERSION    AX255079.1 GI:16074565
KEYWORDS
SOURCE
  ORGANISM
    synthetic construct.
    artificial sequences.
REFERENCE
  AUTHORS      Zohlhofer, D., Brauerle, P., Klein, C. and Neumann, F.J.
  TITLE        Identification of modulators of the interferon gamma signaling
  JOURNAL      pathway and their use in restenosis treatment
  ORGANISM     Patent: WO 0170953-A 18 27-SEP-2001;
  ORGANISM     Micromet AG (DE)
  LOCATION/Qualifiers
    1. 20
      /organism="synthetic construct"
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BASE COUNT      4 a      6 c      5 g      5 t
ORIGIN

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Best Local Similarity 73.3%; Score 11; DB 6; Length 20;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      5 AACGUGAAGAU 15
Db      13 AACGTGAAGAT 3
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RESULT 6
LOCUS AX296064/c 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 7826 from Patent WO0179548.
ACCESSION AX296064
VERSION AX296064.1 GI:17057753
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Barany, F., Zilvri, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
PATENT: WO 0179548-A 7826 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
BASE COUNT 4 a 7 c 4 g 5 t
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Best Local Similarity 64.3%; Pred. No. 2.7e+05;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUACGUGAGAU 15
1 :|||||:
Db 15 GCTACGTCGAGAT 2

RESULT 7
LOCUS AX304787/c 20 bp DNA linear PAT 11-DEC-2001
DEFINITION Sequence 22 from Patent EP1158045.
ACCESSION AX304787
VERSION AX304787.1 GI:17644468
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schneider, Y.J. and Burtiau, N.
TITLE Culture conditions allowing to modulate the expression of cyp3a4 in
JOURNAL caco2 cells
PATENT: EP 1158045-A 22 28-NOV-2001;
UNIVERSITE CATHOLIQUE DE LOUVAIN (BE)
FEATURES
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
BASE COUNT 5 a 4 c 4 g 7 t
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Best Local Similarity 64.3%; Pred. No. 2.7e+05;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUACGUGAGAU 15
1 :|||||:
Db 20 GCTACGTCGAGAT 7

RESULT 8
LOCUS AX349237/c 16 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 21 from Patent WO0202810.
ACCESSION AX349237

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VERSION AX349237.1 GI:18615269
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bickel, R., Ehrlich, R., Ellinger, T., Ernaut, E., Kaiser, T.,
Schulz, T. and Wagner, G.
TITLE Method for qualitative and/or quantitative detecting of molecular
JOURNAL interactions on probe arrays
PATENT: WO 0202810-A 21 10-JAN-2002;
Clondiaag Chip Technologies GmbH (DE)
FEATURES
source 1..16
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/db_xref="taxon:32630"
/note="Oligonucleotide"
BASE COUNT 3 a 5 c 2 g 6 t
ORIGIN
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Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 UACGUGAGAU 15
1 :|||||:
Db 13 TAACGTCGAGAT 2

RESULT 9
LOCUS AX272471/c 17 bp mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 40 from Patent WO0162911.
ACCESSION AX272471
VERSION AX272471.1 GI:16545208
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswigen, J.A., Hamblin, P.A. and
Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 40 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 6 a 5 c 2 g 4 t
ORIGIN
Query Match 69.3%; Score 10.4; DB 6; Length 17;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 UACGUGAGAU 15
1 :|||||:
Db 16 TAACGTCGAGAT 5

RESULT 10
LOCUS AX272472/c 17 bp mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 41 from Patent WO0162911.
ACCESSION AX272472
VERSION AX272472.1 GI:16545209
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mowiggen,J.A., Hamblin,P.A. and
          Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 41 30-AUG-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
SOURCE Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 7 a 4 c 2 g 4 t
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Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 15 TAACGTGAAGCT 4

RESULT 11
LOCUS AX272653/c 17 bp mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 222 from Patent WO0162911.
ACCESSION AX272653
VERSION AX272653.1 GI:16545390
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mowiggen,J.A., Hamblin,P.A. and
          Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 222 30-AUG-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
SOURCE Location/Qualifiers
1. 17
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/db_xref="taxon:9606"
BASE COUNT 6 a 5 c 2 g 4 t
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Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 UAACGUGAAGAU 15
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Db 17 TAACGTGAAGCT 6

RESULT 12
LOCUS AX272654/c 17 bp mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 223 from Patent WO0162911.
ACCESSION AX272654
VERSION AX272654.1 GI:16545391
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mowiggen,J.A., Hamblin,P.A. and
          Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 223 30-AUG-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
SOURCE Location/Qualifiers

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SOURCE 1. 17
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Query Match 69.3%; Score 10.4; DB 6; Length 17;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 UAACGUGAAGAU 15
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Db 14 TAACGTGAAGCT 3

RESULT 13
LOCUS AX272993/c 17 bp mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 562 from Patent WO0162911.
ACCESSION AX272993
VERSION AX272993.1 GI:16545730
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mowiggen,J.A., Hamblin,P.A. and
          Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 562 30-AUG-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
SOURCE Location/Qualifiers
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/organism="Homo sapiens"
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Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 UAACGUGAAGAU 15
:||||:||||:
Db 12 TAACGTGAAGCT 1

RESULT 14
LOCUS AX299883 17 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 24 from Patent WO0183790.
ACCESSION AX299883
VERSION AX299883.1 GI:17129374
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Conner,T.W., Dubois,P., Malven,M. and Masucci,J.D.
TITLE Plant regulatory sequences for selective control of gene expression
JOURNAL Monsanto Technology LLC (US)
FEATURES SOURCE
1. 17
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Fully synthesized Primer"
BASE COUNT 1 a 6 c 4 g 6 t
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Best Local Similarity 83.3%; Pred. No. 4.6e+05;

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Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAUAGCGAG 13
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 Db 16 GACACGTGAG 5

RESULT 15

AX325561

LOCUS AX325561

17 bp DNA

linear

PAT 07-JAN-2002

DEFINITION Sequence 1699 from Patent WO0192512.

ACCESSION AX325561

VERSION AX325561.1 GI:18096318

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris.

Beta vulgaris.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Caryophyllaceae; Beta.

1

REFERENCE

AUTHORS

TITLE

JOURNAL

Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.

Targeted chromosomal genomic alterations in plants using modified

single stranded oligonucleotides

Patent: WO 0192512-A 1699 06-DEC-2001;

UNIVERSITY OF DELAWARE (US)

Location/Qualifiers

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/organism="Beta vulgaris"

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BASE COUNT 6 a 0 c 5 g 6 t

ORIGIN

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Best Local Similarity 75.0%; Pred. No. 4.6e+05;

Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAA 12

|||:|||||

Db 4 AGATAATGTGAA 15

Search completed: May 22, 2003, 19:36:39

Job time : 876.364 secs

GenCore version 5.1.4-P5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 16:52:30 ; Search time 146.364 Seconds
(without alignments)
230.795 Million cell updates/sec

Title: US-09-780-929-97

Sequence: 1 agauaacgugaagau 15

Scoring table: IDENTITY NUC
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Total number of hits satisfying chosen parameters: 1367302

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	22	AA512347
2	12	80.0	17	20	AA18478
3	12	80.0	17	24	ABK26343
4	12	80.0	17	24	ABK26344
5	11.4	76.0	13	23	ABF31424
6	11.4	76.0	13	23	ABF31425
7	11.4	76.0	13	23	ABF76054
8	11.4	76.0	13	23	ABF76055
9	11.4	76.0	20	20	AA203321

C	10	11	73.3	12	23	AB125946	Oligonucleotide pr
C	11	11	73.3	12	23	AB178740	Oligonucleotide pr
C	12	11	73.3	13	23	ABF60400	Oligonucleotide SE
C	13	11	73.3	13	23	ABF60401	Oligonucleotide SE
C	14	11	73.3	20	22	AA166878	Nucleotide sequenc
C	15	11	73.3	20	22	AAAD1670	Desmin PCR primer
C	16	10.8	72.0	15	21	AAV03493	Synthetic oligonuc
C	17	10.8	72.0	18	19	AAV03676	Human Jagged DNA 5
C	18	10.8	72.0	20	18	AAV93936	Primer for exon 24
C	19	10.8	72.0	20	24	ABK2365	Human MDR3 RT-PCR
C	20	10.8	72.0	20	24	ABK2365	Human MDR3 RT-PCR
C	21	10.4	69.3	12	23	AB126106	Capture oligonucle
C	22	10.4	69.3	12	23	AB102382	Oligonucleotide pr
C	23	10.4	69.3	12	23	AB132691	Oligonucleotide pr
C	24	10.4	69.3	12	23	AB134918	Oligonucleotide pr
C	25	10.4	69.3	13	23	AB145308	Oligonucleotide pr
C	26	10.4	69.3	13	23	ABC89900	Oligonucleotide SE
C	27	10.4	69.3	13	23	ABC89901	Oligonucleotide SE
C	28	10.4	69.3	13	23	ABF01726	Oligonucleotide SE
C	29	10.4	69.3	13	23	ABF01727	Oligonucleotide SE
C	30	10.4	69.3	16	24	AAK8514	Oligonucleotide SE
C	31	10.4	69.3	17	21	AAK8514	Nucleic acid quant
C	32	10.4	69.3	17	21	AAK8514	Hammerhead ribozym
C	33	10.4	69.3	17	24	ABK26339	Increased starch p
C	34	10.4	69.3	17	24	ABK26340	Increased starch p
C	35	10.4	69.3	19	24	AA596503	Primer #21 used in
C	36	10.2	68.0	15	21	AA656526	Nucleotide sequenc
C	37	10.2	68.0	15	21	AA656526	Hepatitis B virus
C	38	10.2	68.0	19	18	AA262836	Substrate for HH r
C	39	10.2	68.0	19	18	AA262836	Hepatitis GB virus
C	40	10.2	68.0	19	21	AAK81934	Probe used to dete
C	41	10.2	68.0	20	20	AAK81934	Human biallelic ma
C	42	10	66.7	20	22	AAK81934	Oligo 3 used in co
C	43	10	66.7	20	22	AAK81934	Primer PAD4.31 to
C	44	10	66.7	12	23	ABH97456	Yeast NORF gene SA
C	45	10	66.7	13	23	ABH97456	Oligonucleotide pr
C	45	10	66.7	13	23	ABH97456	Oligonucleotide SE

ALIGNMENTS

RESULT 1	AA512347	standard; DNA; 15 BP.
ID	AA512347	
AC	AA512347	
DT	21-NOV-2001	(first entry)
DE	DNA encoding deoxyribozyme #7.	
XX	Deoxyribozyme; cytosstatic; endonuclease; RNA cleavage; DNA cleavage;	
KW	gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.	
OS	Synthetic.	
PN	WO200159102-A2.	
PD	16-AUG-2001.	
PF	08-FEB-2001; 2001WO-US04223.	
PR	08-FEB-2000; 2000US-0181360.	
PA	31-MAR-2000; 2000US-0193646.	
XX	(RIBO-) RIBOZYME PHARM INC.	
XX	(UYVA) UNIV YALE.	
PI	Breaker R, Beigelman L, Emilsson G;	
XX	WPI; 2001-536526/59.	
DR	New nucleic acids with endonuclease activity, such as ribozymes and	
XX		
PT		

PT nucleozymes, for modulating gene expression in a plant, mammalian,
bacterial or fungal cell -
XX
PS Claim 49; Page 77; 96pp; English.
XX
CC The invention relates to nucleic acid molecules with endonuclease
CC activity, which are particularly useful for cleavage of RNA or DNA.
CC The nucleic acids are used in a pharmaceutical composition and are used
CC to modulate expression of a gene in a plant, mammalian, bacterial or
CC fungal cell. They are used to cleave a separate nucleic acid, preferably
CC RNA. The nucleic acids are used to inhibit gene expression and/or cell
CC proliferation, and can be used to treat a disease or condition. More
CC than one nucleic acid can be independently targeted to the same or
CC different sites in a cell. The nucleic acids may be used to study DNA.
CC The modifications to the nucleic acids optimises their catalytic activity
CC and can maintain or enhance their activity. They exhibit a high degree
CC of specificity for RNA. The present sequence represents the coding
CC sequence of deoxyribozyme #7 used in the method of the invention.
XX
SQ Sequence 15 BP; 7 A; 1 C; 4 G; 3 U; 0 other;
Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGAUAACGUGAAGAU 15
DB 1 AGAUAACGUGAAGAU 15
|||||
RESULT 2
ID AAA18478 standard; RNA; 17 BP.
XX
AC AAA18478;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human TIE-2 substrate sequence SEQ ID NO:1704.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; halpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiodiroma;
KW tuberculous scleriosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trennauy-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN MO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99MO-US06507.
XX
PR 27-MAR-1998; 98US-0079678.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwigen JA;
XX
DR WPI; 1999-591315/50.
XX
PT Novel ribozymes for modulating the synthesis, expression and/or
XX stability of an mRNA encoding an angiogenic factors -
XX
PS Claim 56; Page 97; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with
CC RNA cleaving activity, which specifically cleave RNA encoded by an aryl

CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23362, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiodiroma of tuberculous scleriosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trennauy-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3.
XX
SQ Sequence 17 BP; 7 A; 2 C; 6 G; 2 U; 0 other;
Query Match 80.0%; Score 12; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGAUAACGUGAA 12
DB 5 AGAUAACGUGAA 16
|||||
RESULT 3
ID ABR26343
XX
AC ABR26343;
XX
DT 09-APR-2002 (first entry)
XX
DE Increased starch production genome altering oligonucleotide #195.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyric herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linoleic acid production;
KW photosynthetic process.
XX
OS Beta vulgaris.
XX
PN Synthetic.
XX
PD WO200192512-A2.
XX
PF 06-DEC-2001.
XX
PT 01-JUN-2001; 2001WO-US17672.
XX
PR 01-JUN-2000; 2000US-208538P.
XX
PR 30-OCT-2000; 2000US-244889P.
XX
PR 27-MAR-2001; 2001US-0818875.
XX
XX (UYDE) UNIV DELAWARE.

PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
PS Claim 1; SEQ ID 131422; 29pp + Sequence Listing; German.
XX
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABH00010-ABH99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABH00010-ABH82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 2 A; 5 C; 1 G; 5 T; 0 other;
SQ
Query Match 76.0%; Score 11.4; DB 23; Length 13;
Best Local Similarity 76.9%; Pred. No. 6.8e+03;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0
OY 1 AGNAAACGUGAAG 13
Db 13 AGATAACGTGAGG 1
RESULT 7
ABF76054
ID ABF76054 standard; DNA; 13 BP.
XX
XX ABF76054;
XX
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 176051 for detecting SNP TSC0043704.
DE
XX
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX MO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001MO-IB00713.
PF
XX
XX 07-APR-2000; 2000DE-1019173.
PR
XX
XX (EPig-) EPIGENOMICS AG.
PA
XX
XX Olek A. Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX
XX
XX Claim 1; SEQ ID 176051; 29pp + Sequence Listing; German.
CC
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABH00010-ABH99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABH00010-ABH82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 2 A; 5 C; 1 G; 5 T; 0 other;
SQ

DE Oligonucleotide primer SEQ ID NO 325919 for detecting SNP TSC0032801.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX
 PS Claim 1; SEQ ID 325919; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989 and
 CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX
 SQ Sequence 12 BP; 2 A; 4 C; 1 G; 5 T; 0 other;
 XX
 Query Match 73.3%; Score 11; DB 23; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.1e+04;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAUAACGUGA 11
 Db 12 AGATTAACGTGA 2
 ||:||||:|
 ||:||||:|
 RESULT 11
 AB18740
 ID AB18740 standard; DNA; 12 BP.
 XX
 AC AB18740;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 378713 for detecting SNP TSC0006271.
 XX
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB00713.

XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX
 PS Claim 1; SEQ ID 378713; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989 and
 CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX
 SQ Sequence 12 BP; 5 A; 1 C; 3 G; 3 T; 0 other;
 XX
 Query Match 73.3%; Score 11; DB 23; Length 12;
 Best Local Similarity 81.8%; Pred. No. 1.1e+04;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 AUAACGUGAG 13
 Db 1 AUAACGTGAAG 11
 ||:||||:|
 ||:||||:|
 RESULT 12
 ABF60400
 ID ABF60400 standard; DNA; 13 BP.
 XX
 AC ABF60400;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 160397 for detecting SNP TSC0040381.
 XX
 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX

PS Claim 1: SEQ ID 160397; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 13 BP; 6 A; 1 C; 3 G; 3 T; 0 other;

Query Match 73.3%; Score 11; DB 23; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.1e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 AUACGUGAG 13
1:|||||1111
2 ATACGTCGAG 12
DB

RESULT 13
ABF60401/c
ID ABF60401 standard; DNA; 13 BP.
AC ABF60401;
XX
XX 22-FEB-2002 (first entry)
DT
XX
DE Oligonucleotide SEQ ID NO 160398 for detecting SNP TSC0040381.
XX
XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB00713.
PF
XX
XX 07-APR-2000; 2000DE-1019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
XX Claim 1: SEQ ID 160398; 29pp + Sequence Listing; German.
PS
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 13 BP; 3 A; 3 C; 1 G; 6 T; 0 other;

Query Match 73.3%; Score 11; DB 23; Length 13;
Best Local Similarity 81.8%; Pred. No. 1.1e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 AUACGUGAG 13
1:|||||1111
12 ATACGTCGAG 2
DB

RESULT 14
AAI66878/c
ID AAI66878 standard; DNA; 20 BP.
AC AAI66878;
XX
XX 07-JAN-2002 (first entry)
DT
XX
DE Nucleotide sequence of primer seq id No. 18.
XX
XX Nucleic acid amplification; hybridization assay; interaction assay;
KW expression cloning; PCR primer; ss.
XX
XX Synthetic.
OS
XX
XX WO200171027-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-EP03311.
PF
XX
XX 24-MAR-2000; 2000EP-0106450.
PR
XX
XX (MICR-) MICROMET AG.
PA
XX
XX Zohlhoefer D, Klein C;
PI
XX
XX WPI; 2001-611514/70.
DR
XX
XX A method for the amplification of mRNA from a sample, e.g. for the
PT preparation of in vitro surrogates for pathologically modified cells or
PT tissues
XX
XX Examples; Page 168; 170pp; English.
PS
XX
XX The invention provides a novel method for the amplification of mRNA from
CC a sample. The method comprises (1) generating cDNA from polyadenylated
CC RNA employing at least 1 primer hybridizing to the polyadenylated RNA and
CC comprising a 5' poly(C) or a 5' poly(G) flank; (2) (either: (a)
CC (optionally): (1) (if present) removing non-hybridised, surplus primer(s)
CC and/or surplus dNTPs; (1b) 3' tailing of the generated cDNA with a poly
CC (G) tail when in step (1) primer(s) comprising a 5' poly(C) flank was/
CC were employed or a poly(C) tail when in step (1) primer(s) comprising a
CC 5' poly(G) flank was/were employed; or (b) (optionally) 3' tailing of the
CC generated cDNA with a poly(G) tail when in step (1) primer(s) comprising
CC a 5' poly(C) flank was/were employed or a poly(C) tail when in step (1)
CC primer(s) comprising a 5' poly(G) flank was/were employed using an RNA-
CC ligase, irrespective of the presence or absence of surplus primer(s) and
CC /or surplus dNTPs; and (3) amplifying the tailed cDNA with a primer
CC hybridizing to the tails generated in step (2a) or (2b). The amplified
CC cDNA obtained may be used for in vitro and/or in vivo expression and
CC preparation of mRNA transcripts (which may then be used in hybridization
CC assays (comprising hybridization to oligonucleotide arrays, cDNA arrays
CC and/or PNA arrays) and/or interaction assays (comprising interactions
CC with carbohydrates, lectins, ribozymes, proteins, peptides, antibodies
CC and/or aptamers)) and for sequence specific PCR, cDNA cloning,
CC subtractive hybridization cloning and/or expression cloning. Sequences
CC AAI6676-890 represent primers used in the method of the invention.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Search completed: May 22, 2003, 19:04:24
 Job time : 148.364 secs

Query Match 73.3%; Score 11; DB 22; Length 20;
 Best Local Similarity 81.8%; Pred. No. 1.2e+04;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 AACGUGAAGAU 15
 ||||:|||||:
 DB 13 AACGTGAAGAT 3

RESULT 15

AAD19670/c
 ID AAD19670 standard; DNA; 20 BP.

AC AAD19670;

DT 18-DEC-2001 (first entry)

DE Desmin PCR primer #2 related to the invention.

KW Inhibitor; interferon-gamma; IFN-gamma signalling pathway; therapy;

KW restenosis; coronary artery; carotid artery; femoralis artery;

KW aorta-coronary vein bypass; arterial bypass; venous bypass;

KW balloon angioplasty; stent implantation; vasotropic; PCR primer; ss.

OS Unidentified.

PN MO200170953-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-EP03312.

PR 24-MAR-2000; 2000EP-0106468.

PA (MICR-) MICROMET AG.

PI Zohlhoefer D, Baueerle P, Klein C, Neumann F;

DR WPI; 2001-616404/71.

PT Use of an inhibitor of the interferon-gamma signalling pathway for

PS Example 5; Page 55; 151pp; English.

CC The present invention relates to the use of an inhibitor of the
 CC interferon-gamma (IFN-gamma) signalling pathway for the preparation of
 CC a pharmaceutical composition for the treatment or prevention of
 CC restenosis. The inhibitor is useful for the preparation of a
 CC pharmaceutical composition useful in treating or preventing restenosis
 CC which include restenosis of coronary arteries, carotid arteries,
 CC femoralis arteries, aorta-coronary vein bypass, arterial bypass,
 CC and/or venous bypass; and restenotic modification, where prevention
 CC of restenotic modification is done before, during and/or after balloon
 CC angioplasty and/or stent implantation and the restenosis or restenotic
 CC modification is in-stent restenosis; and for treating and preventing
 CC restenosis in a subject preferably human. The present sequence is a
 CC desmin PCR primer which is used in aberrant gene expression in human
 CC restenotic tissue used in the exemplification of the invention.

SO Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 73.3%; Score 11; DB 22; Length 20;

Best Local Similarity 81.8%; Pred. No. 1.2e+04;

OY 5 AACGUGAAGAU 15

DB 13 AACGTGAAGAT 3

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 18:32:43 ; Search time 1093.18 Seconds

(without alignments)
222.225 Million cell updates/sec

Title: US-09-780-929-97

Perfect score: 15

Sequence: 1 agaaacgugaaga 15

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 5800

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rdg:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10.2	68.0	19	17	AZ759898 1M0533A08
2	8.8	58.7	19	17	AZ465132 1M0274D24
3	8.6	57.3	19	17	AZ603744 1M0423E15
4	8.6	57.3	20	9	AU254575 AU254575
5	8.4	56.0	20	17	AZ501985 1M0341K05
6	8.2	54.7	19	14	C21102 C21102 HMG5000262

7	8.2	54.7	19	17	AZ436629	AZ436629 1M0224A019
8	8.2	54.7	19	17	AZ658282	AZ658282 1M0535C02
9	8.2	54.7	19	17	AZ983624	AZ983624 2M0264A22
10	8.2	54.7	20	17	AZ583235	AZ583235 1M0378J08
11	7.8	52.0	19	17	AZ331326	AZ331326 1M0059B15
12	7.8	52.0	19	17	AZ345449	AZ345449 1M0080J08
13	7.8	52.0	19	17	AZ445511	AZ445511 1M0080J01
14	7.8	52.0	19	17	AZ345536	AZ345536 1M0080O06
15	7.8	52.0	19	17	AZ345572	AZ345572 1M0080U17
16	7.8	52.0	19	17	AZ346709	AZ346709 1M0082M06
17	7.8	52.0	19	17	AZ346710	AZ346710 1M0082N01
18	7.8	52.0	19	17	AZ368837	AZ368837 1M0119A11
19	7.8	52.0	19	17	AZ414372	AZ414372 1M0188G18
20	7.8	52.0	19	17	AZ447223	AZ447223 1M0244H13
21	7.8	52.0	19	17	AZ447247	AZ447247 1M0244G19
22	7.8	52.0	19	17	AZ510096	AZ510096 1M0354B22
23	7.8	52.0	19	17	AZ510106	AZ510106 1M0354E19
24	7.8	52.0	19	17	AZ638980	AZ638980 1M0499L08
25	7.8	52.0	19	17	AZ954985	AZ954985 2M0220H21
26	7.6	50.7	20	17	AZ403838	AZ403838 1M0171K09
27	7.6	50.7	20	17	AZ462631	AZ462631 1M0269F12
28	7.6	50.7	20	17	AZ476391	AZ476391 1M0295F10
29	7.4	49.3	19	9	AU061154	AU061154 AU061154
30	7.4	49.3	19	13	BM397047	BM397047 5009-0-28
31	7.4	49.3	19	17	AZ496805	AZ496805 1M0333G22
32	7.2	48.0	19	9	AI439934	AI439934 t163c04.x
33	7.2	48.0	19	17	AZ319924	AZ319924 1M0039C15
34	7.2	48.0	19	17	AZ375600	AZ375600 1M0129K06
35	7.2	48.0	20	9	AU011147	AU011147 AU011147
36	7.2	48.0	20	17	AZ641695	AZ641695 1M0504E22
37	7.2	48.0	20	17	AZ807038	AZ807038 2M0069C06
38	7.2	48.0	20	17	AZ835078	AZ835078 2M0129E07
39	7.2	46.7	18	14	C21336	C21336 HMG5000337
40	7.2	46.7	18	14	C21365	C21365 HMG5000515
41	7.2	46.7	18	14	D11637	D11637 HMG000C318
42	7.2	46.7	19	9	AU061154	AU061154 AU061154
43	7.2	46.7	19	17	AZ588918	AZ588918 1M0397J05
44	7.2	46.7	19	17	AZ772819	AZ772819 1M0584F02
45	7.2	46.7	19	17	AZ783477	AZ783477 2M0025D18

ALIGNMENTS

RESULT 1
AZ759898
LOCUS
DEFINITION
1M0553A08F Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0553A08 F, DNA sequence.

ACCESSION
AZ759898
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
house mouse.
GSS.

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

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Plate: 0553   row: A   column: 08
Seq primer: CGTGTGTAACGACGCGCCACT
Class: Plasmid ends
High quality sequence stop: 19.
      location/Qualifiers
FEATURES
    source
        1..19

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Plate: 0274  row: D  column: 24
Seq primer: CACACAGGAAACAGCTATGACCC
Class: plasmid ends
High quality sequence stop: 19.
      location/Qualifiers
1. 19.

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/clone_11b="mouse 10kb plasmid UUC1M library"
 /sex="male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42mv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g114732114[9b]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

```

/clone_11b="mouse 10kb plasmid UUCGM library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g11473211419b1Arl29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

```

Query Match: Similarity 68.0%; Score 10.2; DB 17; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.6e+04;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 AGAUAACGUGAAGAU 15
      1 | | | | | : | | | |
LOCUS   3 AAAAAACGTGAAAT 17

RESULT 2
AZ465132/c
DEFINITION 19 bp DNA linear GSS 04-OCT-2000
LOCUS      clone UGCGIM0274D24 R, DNA sequence.
ACCESSION  AZ465132
VERSION     AZ465132.1 GI:10623257
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 19)
            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly
            M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
            and Wright, D., Weils, R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts

TITLE      Unpublished (2000)
JOURNAL    Contact: Robert B. Weiss
COMMENT    University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00

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Query Match Similarity	75.0%;	Score 8.8;	DB 17;	Length 19;
Best Local Similarity	75.0%;	Pred. No. 4.5e+05;		
Matches	9;	Conservative	1;	Mismatches 2; Indels 0; Gaps 0;
Oy	3	AUACGUGAAGA 14		
Db	12	AAACGTGAAA 1		
RESULT 3				
A2603744				
LOCUS				
DEFINITION		19 bp	DNA	linear
				GSS 13-DEC-2000
ACCESSION		A2603744		
VERSION		1M042315F		Mouse 10kb plasmid U00C1M library Mus musculus genomic clone U00C1M042315 F, DNA sequence.
KEYWORDS		A2603744		
SOURCE		A2603744.1		GI:11725934
ORGANISM		GSS.		
		house mouse.		
		Mus musculus		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)		
REFERENCE		Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
AUTHORS		Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
TITLE		Unpublished (2000)		
JOURNAL		Contact: Robert B. Weiss		
COMMENT		University of Utah Genome Center		
		University of Utah		
		Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA		
		Tel: 801 585 5506		
		Fax: 801 585 7177		
		Email: ddunn@genetics.utah.edu		
		Insert Length: 10000		Std Error: 0.00


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/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/note="Vector: pGEM-T-easy"
BASE COUNT      5 a      3 c      3 g      9 t
ORIGIN

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OY	1	AGAUACGUGAAGAU	15
			: :: :
Db	16	AAAAAGCCTGAAGAT	2
RESULT 5			
AZ501985			
LOCUS			
DEFINITION	AZ501985	20 bp	DNA
	IM0341K03F	Mouse 10kb plasmid U0GC1M library Mus musculus genomic clone U0GC1M0341K05 F, DNA sequence.	linear GSS 05-OCT-2000
ACCESSION	AZ501985		
VERSION	AZ501985.1	GI:10683301	
KEYWORDS	GSS.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 20) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Ringey,A., von Niederhausern,A. and Wright,D., Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

```

FEATURES
Source
      insert length: 1000      Std Error: 0.00
      Plate: 0341      row: K      column: 05
      Seq primer: CGTGTAAACGACGCCACAGT
      Class: plasmid ends
      High quality sequence stop: 20.
      Location/Qualifiers
          1..20
              /organism="Mus musculus"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="U06C1M0341K05"
              /clone_11p="Mouse 10kb plasmid U06C1M library"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pMD42 (g114732114|gplAF129072.1), a copy-number
              inducible derivative of plasmid RL. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to

```

adapored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 56.0%; Score 8.4; DB 17; Length 20;

Best Local Similarity 70.0%; Pred. No. 7.6e+05;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AUAACGUGAA 12

Db 9 ATGACGTGAA 18

RESULT 6 C21102 19 bp mRNA linear EST 23-OCT-1996

LOCUS HUMGS0002625 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA

DEFINITION sequence.

ACCESSION C21102

VERSION C21102.1 GI:1622212

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 19)

Okubo, K. human gene expression database

BodyMap; unpublished (1995)

Contact: Okubo, K.

Institute for Molecular and Cellular Biol

Osaka University

1-3, Yamadaoka, Suita, Osaka Pref. 565, Japan

Tel: 06-877-5111(ex.3315)

Email: kousakueimcb.osaka-u.ac.jp

Human Gene Signature, 3'-directed cDNA sequence. We are not

submitting the same cDNA sequence redundantly to DDBJ since 1993.

For the abundance information of clones with this sequence in this

library and as well as in other 3'-directed libraries, 'see'

http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones

represented by this GS sequences is also found there.

FEATURES

source

1. 19

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Human adult (K.Okubo)"

/dev_stage="adult"

/note="Organ: blood; Vector: 1-gt-11; Site: 1: Eco-RI;

Monocytes were prepared from blood by ficoll-hypaque,

percoll and T cell rosetting purification steps (purity:

96 %). mRNA was prepared from activated monocytes from a

patient with rheumatoid arthritis. mRNA was reverse

transcribed with MolV. Using Eco-RI linker's cDNA was

cloned into 1-gt-11 vector arms. The cDNA library was

screened by differential hybridization using radioactively

marked ss-cDNA from activated and non-activated

monocytes.

BASE COUNT 4 a 5 c 1 g 8 t 1 others

ORIGIN

Query Match 54.7%; Score 8.2; DB 14; Length 19;

Best Local Similarity 53.8%; Pred. No. 9.5e+05;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AUAACGUGAAGAU 15

Db 14 ATAAATGAGGAT 2

RESULT 7 AZ436629

LOCUS AZ436629 19 bp DNA linear GSS 03-OCT-2000

DEFINITION IM0224019f Mouse 10kb plasmid U06C1M library Mus musculus genomic

clone U06C1M0224019 F, DNA sequence.

ACCESSION AZ436629

VERSION AZ436629.1 GI:10560642

KEYWORDS GSS

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0224 row: 0 column: 19

Seq primer: CGTGTAAACGACGCCACGT

Class: plasmid ends

High quality sequence stop: 19.

location/Qualifiers

1. 19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="U06C1M0224019"

/clone_lib="Mouse 10kb plasmid U06C1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (9147321149b1AF129072.1), a copy-number

inducible derivative of plasmid RI. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapored mouse DNA was annealed to

adapored vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 5 a 1 c 8 g 5 t

ORIGIN

Query Match 54.7%; Score 8.2; DB 17; Length 19;

Best Local Similarity 69.2%; Pred. No. 9.5e+05;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAUACGUGAAGA 14

Db 7 GAGAACTGATGA 19

RESULT 8 AZ658282/c

RESULT 9
AZ983624/C

RESULT 10
AZ583235

LOCUS AZ583235 20 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0378J08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0378J08 F, DNA sequence.
 ACCESSION AZ583235
 VERSION AZ583235.1 GI:11702915
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0378 row: J column: 08
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0378J08"
 /clone.lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g114732114[gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 8 a 5 c 3 g 4 t
 ORIGIN

Query Match 54.7%; Score 8.2; DB 17; Length 20;
 Best Local Similarity 61.5%; Pred. No. 9.8e+05;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 AGAUAACGUGAAG 13
 1
 DB 8 AAATACCTGAG 20

RESULT 11
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LOCUS AZ311326 19 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0059B15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0059B15 F, DNA sequence.
 ACCESSION AZ311326
 VERSION AZ311326.1 GI:10393927
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0059 row: B column: 15
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0059B15"
 /clone.lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g114732114[gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 4 a 9 c 0 g 6 t
 ORIGIN

Query Match 52.0%; Score 7.8; DB 17; Length 19;
 Best Local Similarity 63.6%; Pred. No. 1.6e+06;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUAACGUGAA 12
 1
 DB 13 GGTAAAGTGA 3

RESULT 12
 AZ345449/c

LOCUS A2345449 19 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0080108F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0080108 F, DNA sequence.
 ACCESSION A2345449
 VERSION A2345449.1 GI:10424686
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0080 row: I column: 08
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080108"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g114732114[gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 BASE COUNT 4 a 9 c 0 g 6 t
 ORIGIN
 Query Match 52.0%; Score 7.8; DB 17; Length 19;
 Best Local Similarity 63.6%; Pred. No. 1.6e+06;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 GAUAAAGUGAA 12
 1 : 11 1 : 111
 Db 13 GGTAAAGTGAA 3
 RESULT 13
 A2345511/C

LOCUS A2345511 19 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0080101F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0080101 F, DNA sequence.
 ACCESSION A2345511
 VERSION A2345511.1 GI:10424748
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0080 row: J column: 01
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080101"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g114732114[gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 BASE COUNT 4 a 9 c 0 g 6 t
 ORIGIN
 Query Match 52.0%; Score 7.8; DB 17; Length 19;
 Best Local Similarity 63.6%; Pred. No. 1.6e+06;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 GAUAAAGUGAA 12
 1 : 11 1 : 111
 Db 13 GGTAAAGTGAA 3
 RESULT 14
 A2345536/C

LOCUS AZ345536 19 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0080006F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0080006 F, DNA sequence.
 ACCESSION AZ345536
 VERSION AZ345536.1 GI:10424773
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: 0 column: 06
 Seq primer: CGTGTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 FEATURES
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 1. 19
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080006"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g114732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT

4 a 9 c 0 g 6 t

ORIGIN

Query Match 52.0%; Score 7.8; DB 17; Length 19;
 Best Local Similarity 63.6%; Pred. No. 1.6e+06;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUAAACUGAA 12
 1 : 11 1 : 11
 Db 13 GGTAAAGTGAA 3

RESULT 15
 AZ345572/c

LOCUS AZ345572 19 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0080017F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0080017 F, DNA sequence.
 ACCESSION AZ345572
 VERSION AZ345572.1 GI:10424809
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: 0 column: 17
 Seq primer: CGTGTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 FEATURES
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 1. 19
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080017"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g114732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT

4 a 9 c 0 g 6 t

Query Match 52.0%; Score 7.8; DB 17; Length 19;
 Best Local Similarity 63.6%; Pred. No. 1.6e+06;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUAAACUGAA 12
 1 : 11 1 : 11
 Db 13 GGTAAAGTGAA 3

Search completed: May 22, 2003, 20:17:01
 Job time : 1100.18 secs

CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 154
SEQ ID NO: 22
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-780-175-22

Query Match 72.0%; Score 10.8; DB 4; Length 20;
Best Local Similarity 64.3%; Pred. No. 1.8e+03;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAUACGUGAAGAU 15
1 : |||:|||||
Db 20 GCTGACGTGAAGAT 7

RESULT 3
US-08-182-968A-447/C
Sequence 447, Application US/08182968A
Patent No. 5610054

GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,968A
FILING DATE: 13-JANUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,888
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/277
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 447:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-182-968A-447

Query Match 68.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15
|||:|||||
Db 15 AGATAACGACAGAGT 1

RESULT 4
US-08-774-306A-447/C
Sequence 447, Application US/08774306A
Patent No. 5869253

GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,306A
FILING DATE: December 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 447:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-306A-447

Query Match 68.0%; Score 10.2; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15
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Db 15 AGATAACGACAGAGT 1

RESULT 5
US-09-064-156A-447/C
Sequence 447, Application US/09064156A
Patent No. 6132966

GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 498
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles

Query Match 68.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,156A
FILING DATE: April 21, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/774,306
FILING DATE: December 26, 1996
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 447:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-064-156A-447

Query Match 68.0%; Score 10.2; DB 3; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15
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Db 15 AGATAACGACAAAGCT 1

RESULT 6
US-08-580-038-29
Sequence 29, Application US/08580038
Patent No. 5807670
GENERAL INFORMATION:
APPLICANT: Muethoff, A. S.
APPLICANT: Simons, J. N.
APPLICANT: Birkenmeyer, L.
APPLICANT: Leary, T. P.
APPLICANT: Erker, J. C.
APPLICANT: Desai, S. M.
APPLICANT: Mushahwar, I. K.
APPLICANT: Chalmers, M.
APPLICANT: Dawson, G. J.
TITLE OF INVENTION: Detection of Hepatitis GB Virus
TITLE OF INVENTION: Genotypes
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,038
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Foremski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5793.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-0378
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-580-038-29

Query Match 68.0%; Score 10.2; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 3.9e+03;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15
|||:|||||
Db 4 AGAGAGGTTAGAT 18

RESULT 7
US-09-780-175-50/c
Sequence 50, Application US/09780175
Patent No. 6440738
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
FILE REFERENCE: RTS-0164
CURRENT APPLICATION NUMBER: US/09/780,175
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 50
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-780-175-50

Query Match 66.7%; Score 10; DB 4; Length 20;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAAGAU 15
|||:|||||
Db 19 ACGTGAAGAT 10

RESULT 8
US-08-758-306-1325/c
Sequence 1325, Application US/08758306
Patent No. 5807743
GENERAL INFORMATION:
APPLICANT: Slinchcomb, Dan T.
APPLICANT: McSwiggen, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Fastseq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/758,306
 FILING DATE: December 3, 1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Wabburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 212/112
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 1325:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-758-306-1325

Query Match	65.3%	Score 9.8	DB 1	Length 17
Best Local Similarity	76.9%	Pred. No. 6.5e+03		
Matches 10; Conservative		1; Mismatches 2;	Indels 0;	Gaps 0

QY	1	AGAUACGUGAAG	13
		:	
Db	13	AGATAAGGGAAG	1

```

RESULT 9
US-09-205-143-70/c
: Sequence 70, Application US/09205143
: Patent No. 6107091
: GENERAL INFORMATION:
: APPLICANT: Lex M. Covert
: TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-16 EXPRESSION
: FILE REFERENCE: RTS-0032
: CURRENT APPLICATION NUMBER: US/09/205,143
: CURRENT FILING DATE: 1998-12-03
: NUMBER OF SEQ ID NOS: 87
: SEQ ID NO 70
: LENGTH: 18
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-143-70

```

```

Query Match      65.3%   Score 9.8:   DB 3:   Length 18;
Best Local Similarity 76.9%   Pred. No. 6.5e+03;
Matches 10: Conservative 1: Mismatches 2; Indels 0; Gaps 0

```

QY	2	GAUACGUGAGA	14
		:	
Db	18	GAAAAGGTGAGA	6

```

RESULT 10
US-09-561-497-82
Sequence 82: Application US/09561497
Patent No. 6372433
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR OF DNA BINDING-1 EXPRESSION
FILE REFERENCE: RTS-0149
CURRENT APPLICATION NUMBER: US/09/561,497
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 82
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-561-497-82

```

Query Match	65.3%	Score 9.8;	DB 4;	Length 20;
Best Local Similarity	84.6%	Pred. No. 6.5e+03;		
Matches 11; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 2 GAUACGUGAAGA 14
11 1111 1111
Db 6 GAAACGAGAAGA 18

```

11
US-09-844-634-63
; Sequence 63, Application US/09844634
; Patent No. 6410324
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRESSION
; FILE REFERENCE: RRS-0216
; CURRENT APPLICATION NUMBER: US/09/844,634
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-844-634-63

```

Query Match	65.3%	Score 9.8;	DB 4;	Length 20;
Best Local Similarity	69.2%;	Pred. No. 6.5e+03;		
Matches	9;	Conservative	2;	Mismatches 2;
				Indels 0;
				Gaps 0;

QY	1	AGAUACGUGAAG	13
		: :	
Db	2	AGCTACTTGAAG	14

RESULT 12
 US-08-180-2098-5
 Sequence 5, Application US/08180209B
 Patent No. 5593877
 GENERAL INFORMATION:
 APPLICANT: King, Te-Piao
 TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
 TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
 TITLE OF INVENTION: HALAURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED
 TITLE OF INVENTION: THEREON
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESS: Klauder & Jackson
 STREET: 411 Hackensack Avenue

CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,209B
FILING DATE: 11-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-180-209B-5

Query Match
Best Local Similarity 64.0%; Score 9.6; DB 1; Length 17;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAUACGUGAGAU 15
DB 1 GAYACNGTNARAT 14

RESULT 13
US-08-385-745-5
Sequence 5, Application US/08385745
Patent No. 5612209
GENERAL INFORMATION:
APPLICANT: King, Te Piao
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U S A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,745
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/031,400
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 3288-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-385-745-5

Query Match
Best Local Similarity 64.0%; Score 9.6; DB 1; Length 17;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAUACGUGAGAU 15
DB 1 GAYACNGTNARAT 14

RESULT 14
US-08-485-388-5
Sequence 5, Application US/08485388
Patent No. 6270763
GENERAL INFORMATION:
APPLICANT: King, Te Piao
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,388
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/385,745
FILING DATE: 08-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,400
FILING DATE: 11-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 FWCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-485-388-5

Query Match 64.0%; Score 9.6; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 8.3e+03;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 GAUACGUGAGAU 15
||| | : ||| :
DB 1 GAYACGCTNARAT 14

RESULT 15

US-08-474-853-5
; Sequence 5, Application US/08474853
; Patent No. 6287559

GENERAL INFORMATION:

APPLICANT: King, Te-Piao

TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF

TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND

TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,853

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/180,209

FILING DATE: 11-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/031,400

FILING DATE: 11-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-074 CIPB

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ. ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-474-853-5

OY 2 GAUACGUGAGAU 15

||| | : ||| :
DB 1 GAYACGCTNARAT 14

Query Match 64.0%; Score 9.6; DB 4; Length 17;

Best Local Similarity 50.0%; Pred. No. 8.3e+03;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Job time : 35.2727 secs

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 19:36:48 ; Search time 70.9091 Seconds

(Without alignments)
279.329 Million cell updates/sec

Title: US-09-780-929-97
Sequence: 15
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 191488

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	US-09-780-929-97	Sequence 97, Appl
2	10.8	72.0	17	US-09-730-2898-606	Sequence 606, App
3	10.8	72.0	17	US-09-730-2898-607	Sequence 607, App
4	10.8	72.0	18	US-10-213-329-4	Sequence 4, Appl
5	10.4	69.3	19	US-09-969-373-2697	Sequence 2697, Ap
6	10.2	68.0	15	US-09-504-231A-469	Sequence 469, App
7	10.2	68.0	15	US-09-274-553D-469	Sequence 469, App
8	10.2	68.0	19	US-10-000-773A-6	Sequence 6, Appl
9	9.8	65.3	17	US-09-776-474-739	Sequence 739, App
10	9.8	65.3	17	US-09-776-474-959	Sequence 959, App
11	9.8	65.3	20	US-09-918-187-64	Sequence 64, Appl
12	9.8	65.3	20	US-09-800-631-141	Sequence 141, App
13	9.4	62.7	17	US-09-730-2898-596	Sequence 596, App
14	9.4	62.7	18	US-09-878-582-29	Sequence 29, Appl
15	9.4	62.7	18	US-09-969-373-4497	Sequence 4497, Ap
16	9.4	62.7	19	US-09-969-373-1862	Sequence 1862, Ap
17	9.4	62.7	20	US-09-917-963-42	Sequence 42, Appl
18	9.4	62.7	20	US-09-953-611-56	Sequence 56, Appl
19	9.4	62.7	20	US-09-752-983-112	Sequence 112, App

C	20	9.4	62.7	20	US-09-908-500A-15	Sequence 15, Appl
	21	9.2	61.3	15	US-09-825-805-150	Sequence 150, Appl
	22	9.2	61.3	15	US-09-365-029-87	Sequence 87, Appl
	23	9.2	61.3	15	US-09-365-029-88	Sequence 88, Appl
	24	9.2	61.3	16	US-09-365-029-5	Sequence 11, Appl
C	25	9.2	61.3	16	US-09-365-029-11	Sequence 25, Appl
	26	9.2	61.3	17	US-08-908-884-25	Sequence 525, App
	27	9.2	61.3	17	US-09-825-805-525	Sequence 103, App
	28	9.2	61.3	17	US-09-730-2898-103	Sequence 833, App
	29	9.2	61.3	17	US-09-730-2898-835	Sequence 1081, Ap
	30	9.2	61.3	17	US-09-730-2898-1081	Sequence 935, App
	31	9.2	61.3	17	US-09-848-754A-935	Sequence 936, App
	32	9.2	61.3	17	US-09-848-754A-936	Sequence 2185, Ap
	33	9.2	61.3	17	US-09-848-754A-2185	Sequence 74, Appl
	34	9.2	61.3	17	US-09-776-474-74	Sequence 426, App
	35	9.2	61.3	17	US-09-776-474-426	Sequence 427, App
	36	9.2	61.3	17	US-09-776-474-427	Sequence 25, Appl
	37	9.2	61.3	17	US-09-908-323-25	Sequence 89, Appl
	38	9.2	61.3	18	US-09-922-598-89	Sequence 89, Appl
	39	9.2	61.3	18	US-09-805-761-22	Sequence 22, Appl
	40	9.2	61.3	18	US-09-889-292A-89	Sequence 89, Appl
	41	9.2	61.3	18	US-09-889-735-89	Sequence 89, Appl
	42	9.2	61.3	18	US-09-900-444-89	Sequence 89, Appl
	43	9.2	61.3	18	US-09-989-730-89	Sequence 89, Appl
	44	9.2	61.3	18	US-09-990-436-89	Sequence 89, Appl
	45	9.2	61.3	18	US-09-991-181-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-09-780-929-97
Sequence 97, Application US/09780929
Patent No. US20020151693A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: Breaker, Ronald
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MHHB00-884-H (500/001)
CURRENT APPLICATION NUMBER: US/09/780, 929
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: US 60/181,360
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PatentIn version 3.0
SEQ ID NO 97
LENGTH: 15
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-780-929-97
Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAUAACGUGAAGAU 15
Db 1 AGAUAACGUGAAGAU 15

RESULT 2
US-09-730-2898-606/c
Sequence 606, Application US/097302898
Publication No. US20030050259A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease

FILE REFERENCE: MBH00-864-A (400/006)
CURRENT APPLICATION NUMBER: US/09/730,289B
CURRENT FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/169,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 3897
SOFTWARE: PatentIn version 3.0
SEQ ID NO 606
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-730-289B-606

Query Match 72.0%; Score 10.8; DB 9; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.3e+04;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAGA 14
DB 17 AGATAACATGAGAGA 4

RESULT 3
US-09-730-289B-607/C
Sequence 607, Application US/09730289B
Publication No. US20030050259A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
FILE REFERENCE: MBH00-864-A (400/006)
CURRENT APPLICATION NUMBER: US/09/730,289B
CURRENT FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/169,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 3897
SOFTWARE: PatentIn version 3.0
SEQ ID NO 607
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-730-289B-607

Query Match 72.0%; Score 10.8; DB 9; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.3e+04;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAGA 14
DB 15 AGATAATGTGAGAGA 2

RESULT 4
US-10-213-329-4
Sequence 4, Application US/10213329
Publication No. US20030083465A1
GENERAL INFORMATION:
APPLICANT: Zimrin, Ann B.
APPLICANT: Maciej, Thomas
APPLICANT: Wong, Michael K.K.
APPLICANT: Pepper, Michael S.
APPLICANT: Montesano, Roberto
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS
TITLE OF INVENTION: BASED ON JAGGED/NOTCH PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: 0036-101
CURRENT APPLICATION NUMBER: US/10/213,329
CURRENT FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: US/09/199,865
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/018,841
PRIOR FILING DATE: 1996-05-31
PRIOR APPLICATION NUMBER: PCT/US97/09407

PRIOR FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cDNA
US-10-213-329-4

Query Match 72.0%; Score 10.8; DB 9; Length 18;
Best Local Similarity 71.4%; Pred. No. 1.3e+04;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAUAACGUGAGAU 15
DB 1 GAGACCGTGAAGAT 14

RESULT 5
US-09-969-373-2697/C
Sequence 2697, Application US/09969373
Patent No. US20020133852A1
GENERAL INFORMATION:
APPLICANT: Efferitz, Roger J.
APPLICANT: Haug, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 2697
LENGTH: 19
TYPE: DNA
ORGANISM: Glycine max
US-09-969-373-2697

Query Match 69.3%; Score 10.4; DB 10; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.1e+04;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAA 12
DB 17 AGACAACGTGAA 6

RESULT 6
US-09-504-231A-469/C
Sequence 469, Application US/09504231A
Patent No. US20020013458A1
GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Pavco, Pamela
APPLICANT: Maciej, Dennis
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILE REFERENCE: rpl 247/282
CURRENT APPLICATION NUMBER: US/09/504,231A
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 09/274,553
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/257,608
PRIOR FILING DATE: 1999-02-24

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; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 469
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-469

Query Match
Best Local Similarity 68.0%; Score 10.2; DB 10; Length 15;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGUAAACGUGAAGAU 15
DB 15 AGATAACGACAGGT 1

RESULT 7
US-09-274-553D-469/c
; Sequence 469, Application US/09274553D
; Patent No. US2002082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwigen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 469
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-469

Query Match
Best Local Similarity 68.0%; Score 10.2; DB 10; Length 15;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGUAAACGUGAAGAU 15
DB 15 AGATAACGACAGGT 1

RESULT 8
US-10-000-773A-6
; Sequence 6, Application US/10000773A
; Publication No. US20030069195A1
; GENERAL INFORMATION:
; APPLICANT: Farrar, Gwenyth Jane
; APPLICANT: Humphries, Peter
; APPLICANT: Kenna, Paul
; APPLICANT: Millington-Ward, Sophia
; TITLE OF INVENTION: Suppression of Polymorphic Alleles
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; FILE REFERENCE: MGR-001CP
; CURRENT APPLICATION NUMBER: US/10/000,773A
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/142,125
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: PCT/GB97/00574
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: GB 9604449.0
; PRIOR FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' human collagen 1A2 primer
US-10-000-773A-6

Query Match
Best Local Similarity 68.0%; Score 10.2; DB 9; Length 19;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAGAU 15
DB 2 AGAGATGCTGAAGAT 16

RESULT 9
US-09-776-474-739
; Sequence 739, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Booher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, All
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 739
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-739

Query Match
Best Local Similarity 84.6%; Score 9.8; DB 9; Length 17;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAUAACGUGAAG 13
DB 2 AGAAAUUGUGAAG 14

RESULT 10
US-09-776-474-959
; Sequence 959, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Booher, Robert
```



```

; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 959
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-959

Query Match
Best Local Similarity 65.3%; Score 9.8; DB 9; Length 17;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGAUAACGUGAG 13
    |||||
DB 4 AGAAAUUGUGAG 16

RESULT 11
US-09-918-187-64
; Sequence 64, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590
; CURRENT APPLICATION NUMBER: US/09/918,187
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-64

Query Match
Best Local Similarity 65.3%; Score 9.8; DB 9; Length 20;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 AUAACGUGAGAU 15
    |||||
DB 4 ATATCTGAAGAT 16

RESULT 12
US-09-800-631-141/C
; Sequence 141, Application US/09800631
; Patent No. US20020082228A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXPR
; FILE REFERENCE: ISPH-0544
; CURRENT APPLICATION NUMBER: US/09/800,631
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 141
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-800-631-141

Query Match
Best Local Similarity 65.3%; Score 9.8; DB 10; Length 20;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGAUAACGUGAG 13
    |||||
DB 13 AGATAACATGTAG 1

RESULT 13
US-09-730-289B-596
; Sequence 596, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blact, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 596
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-596

Query Match
Best Local Similarity 62.7%; Score 9.4; DB 9; Length 17;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 AUAACGUGAG 13
    |||||
DB 4 AUAACAUGAG 14

RESULT 14
US-09-878-582-29/C
; Sequence 29, Application US/09878582
; Patent No. US20020058638A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowseart
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION
; FILE REFERENCE: ISPH-0463
; CURRENT APPLICATION NUMBER: US/09/878,582
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/577,902
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/358,381
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US99/29594,
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-878-582-29
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Query Match 62.7%; Score 9.4; DB 10; Length 18;
Best Local Similarity 72.7%; Pred. No. 7.3e+04;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 AACGUGAAGAU 15
||:|||||:
Db 17 AAGGTGAAGAT 7

RESULT 15

US-09-969-373-4497/C
; Sequence 4497, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 4497
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-969-373-4497

Query Match 62.7%; Score 9.4; DB 10; Length 18;
Best Local Similarity 72.7%; Pred. No. 7.3e+04;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 GAUACGUGAA 12
||:|||||:
Db 13 GATAACGTGCA 3

Search completed: May 22, 2003, 21:38:46
Job time : 72.9091 secs

Query Match 72.0%; Score 10.8; DB 65; Length 18;
Best Local Similarity 64.3%; Pred. No. 1e+05;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAUACGUGAAGAU 15
11:1111111111
DB 2 GATACCTGAAGAT 15

RESULT 13
PCT-US02-03159-22/c
Sequence 22, Application PC/TUS0203159
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Robert McKay
APPLICANT: Susan M. Preler
APPLICANT: Jacqueline Waitt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
FILE REFERENCE: RISP-0270
CURRENT APPLICATION NUMBER: PCT/US02/03159
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 22
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-03159-22

Query Match 72.0%; Score 10.8; DB 1; Length 20;
Best Local Similarity 64.3%; Pred. No. 1e+05;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAUACGUGAAGAU 15
11:1111111111
DB 20 GCTGACGTGAAGAT 7

RESULT 14
US-09-068-506-50/c
Sequence 50, Application US/09068506A
GENERAL INFORMATION:
APPLICANT: YASGE, Hirofumi
APPLICANT: YOSHIMURA, Kunamoto
TITLE OF INVENTION: DIAGNOSIS OF DISEASES ASSOCIATED WITH CORONARY
FILE REFERENCE: 0032-245P
CURRENT APPLICATION NUMBER: US/09/068,506A
CURRENT FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-068-506-50

Query Match 72.0%; Score 10.8; DB 14; Length 20;
Best Local Similarity 64.3%; Pred. No. 1e+05;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAUACGUGAAGAU 15
11:1111111111
DB 14 GGTACCTGAAGAT 1

RESULT 15
US-09-514-000-12603/c
Sequence 12603, Application US/09514000

GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)B
CURRENT APPLICATION NUMBER: US/09/514,000
CURRENT FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 15034
SEQ ID NO 12603
LENGTH: 20
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
US-09-514-000-12603

Query Match 72.0%; Score 10.8; DB 19; Length 20;
Best Local Similarity 64.3%; Pred. No. 1e+05;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAUACGUGAAGAU 15
11:1111111111
DB 20 GATGACCTGAAGAT 7

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Job time: 1731.64 secs

GenCore version 5.1.4-P5.4578
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OW nucleic - nucleic search, using sw model

Run on: May 22, 2003, 19:04:38 ; Search time 371.364 Seconds
(Without alignments)
209.509 Million cell updates/sec

Title: US-09-780-929-97

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6438716 seqs, 2593467500 residues

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Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq2:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	11.8	78.7	20	9	US-10-316-389-88
C 2	11.4	76.0	20	1	PCT-US02-38622-50
C 3	11	73.3	15	9	US-10-287-818-374
C 4	11	73.3	15	9	US-10-287-818-374
C 5	10.8	72.0	19	9	US-10-310-188-47798
C 6	10.8	72.0	20	9	US-10-302-027-46
C 7	10.8	72.0	20	9	US-10-302-027-46
C 8	10.4	69.3	16	8	US-10-311-109-21
C 9	10.4	69.3	17	6	US-09-846-903-24
C 10	10.4	69.3	17	6	US-10-310-188-80491
C 11	10.4	69.3	19	1	PCT-US03-03662-97
C 12	10.4	69.3	19	1	PCT-US03-03662-336
C 13	10.4	69.3	19	9	US-10-310-188-14089
C 14	10.4	69.3	20	1	PCT-US02-38806-82
C 15	10.4	69.3	20	8	US-10-317-277A-73
C 16	10.4	69.3	20	8	US-10-317-277A-148
C 17	10.2	68.0	15	6	US-09-274-553E-469
C 18	10.2	68.0	17	9	US-10-310-188-22900
C 19	10.2	68.0	19	1	PCT-US02-34679-118
C 20	10.2	68.0	19	9	US-10-287-174-118
C 21	10.2	68.0	19	9	US-10-293-338-4500
C 22	10.2	68.0	19	9	US-10-349-143-4165

C 23	10.2	68.0	20	9	US-10-298-994-110	Sequence 110, App
C 24	10.2	68.0	20	9	US-10-298-994-212	Sequence 112, App
C 25	10.2	68.0	20	9	US-10-310-188-35003	Sequence 35003, A
C 26	10.2	68.0	20	9	US-10-317-249-86	Sequence 86, Appl
C 27	10.2	68.0	20	9	US-10-317-249-161	Sequence 161, App
C 28	10	66.7	15	1	PCT-US02-28539-2145	Sequence 2145, App
C 29	10	66.7	15	1	PCT-US02-28539-2146	Sequence 2146, App
C 30	10	66.7	15	1	PCT-US02-28539-3267	Sequence 3267, App
C 31	10	66.7	15	8	US-10-287-787-13654	Sequence 13654, A
C 32	10	66.7	15	9	US-10-305-276-1129	Sequence 1129, App
C 33	10	66.7	15	9	US-10-316-954-4481	Sequence 4481, App
C 34	10	66.7	15	9	US-10-316-954-5747	Sequence 5747, App
C 35	10	66.7	15	9	US-10-305-276A-1129	Sequence 1129, App
C 36	10	66.7	15	9	US-10-364-516-2145	Sequence 2145, App
C 37	10	66.7	15	9	US-10-364-516-2146	Sequence 2146, App
C 38	10	66.7	15	9	US-10-364-516-3267	Sequence 3267, App
C 39	10	66.7	15	9	US-10-364-516-3268	Sequence 3268, App
C 40	10	66.7	15	9	US-10-364-516-3268	Sequence 3268, App
C 41	10	66.7	15	9	US-10-385-163-94	Sequence 1165, App
C 42	10	66.7	19	8	US-10-385-163-94	Sequence 94, Appl
C 43	10	66.7	19	11	US-60-453-420-94	Sequence 94, Appl
C 44	9.8	65.3	15	9	US-10-305-273-723	Sequence 723, App
C 45	9.8	65.3	15	9	US-10-305-273-1246	Sequence 1246, App

ALIGNMENTS

RESULT 1
US-10-316-389-88/c
Sequence 88, Application US/10316389
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF ABC2 EXPRESSION
FILE REFERENCE: PRT-0382
CURRENT APPLICATION NUMBER: US/10/316, 389
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 143
SEQ ID NO 88
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-316-389-88

Query Match 78.7% Score 11.8; DB 9; Length 20;
Best Local Similarity 80.0% Pred. No. 1.1e+04;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

0Y 1 AGAUAACGUGAAGAU 15
Db 15 AGACACGGGAAGAT 1
RESULT 2
PCT-US02-38622-50/c
Sequence 50, Application PC/TUS0238622
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freiler
TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
FILE REFERENCE: RSP-0447
CURRENT APPLICATION NUMBER: PCT/US02/38622
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 10/003, 919
PRIOR FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 50
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence

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FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-38622-50

Query Match
Best Local Similarity 76.0%; Score 11.4; DB 1; Length 20;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GAUACGUGAAGA 14
    |||:|||||
Db 20 GACACGTGAGA 8

RESULT 3
US-10-287-818-374
; Sequence 374, Application US/10287818
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Vibrio cholerae chromosome I, complete chromosome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,818
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 1318
; SOFTWARE: Proprietary
; SEQ ID NO 374
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Vibrio cholerae chromosome I, complete chromosome.
; FEATURE:
; LOCATION: (810101)...(810115)
; OTHER INFORMATION: Chromosome - 1 strand - positive ConnectonbjectNumber = 534
US-10-287-818-374

Query Match
Best Local Similarity 73.3%; Score 11; DB 9; Length 15;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 AACGUGAAGAU 15
    |||:|||||
Db 1 AACGTGAAGAT 11

RESULT 4
US-10-287-818-836
; Sequence 836, Application US/10287818
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Vibrio cholerae chromosome I, complete chromosome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,818
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 1318
; SOFTWARE: Proprietary
; SEQ ID NO 836
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Vibrio cholerae chromosome I, complete chromosome.
; FEATURE:
; LOCATION: (1812221)...(1812235)
; OTHER INFORMATION: Chromosome - 1 strand - negative ConnectonbjectNumber = 1169
US-10-287-818-836

Query Match
Best Local Similarity 73.3%; Score 11; DB 9; Length 15;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 AACGUGAAGAU 15
    |||:|||||
Db 1 AACGTGAAGAT 11

RESULT 5
US-10-310-188-47798
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```
; Sequence 47798, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: Rosettacomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent version 3.1
; SEQ ID NO 47798
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-47798

Query Match
Best Local Similarity 72.0%; Score 10.8; DB 9; Length 19;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUACGUGAAGAU 15
    |||:|||||
Db 2 GAGACATGAGAT 15

RESULT 6
US-10-302-027-46/c
; Sequence 46, Application US/10302027
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION
; FILE REFERENCE: PTS-0068
; CURRENT APPLICATION NUMBER: US/10/302,027
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-302-027-46

Query Match
Best Local Similarity 72.0%; Score 10.8; DB 9; Length 20;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 GAUACGUGAAGAU 15
    |||:|||||
Db 14 GGTACTTGAAGAT 1

RESULT 7
US-10-302-027-106
; Sequence 106, Application US/10302027
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION
; FILE REFERENCE: PTS-0068
; CURRENT APPLICATION NUMBER: US/10/302,027
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-302-027-106

Query Match
Best Local Similarity 72.0%; Score 10.8; DB 9; Length 20;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

US-10-310-188-47798
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Matches: 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAUACGUGAAG 15
1 :|||:|||||
Db 7 GGTAATTGAAGAT 20

RESULT 8
US-10-331-109-21/c
; Sequence 21, Application US/10331109
; GENERAL INFORMATION:
; APPLICANT: Bickel, et al.
; TITLE OF INVENTION: Method for the qualitative and/or quantitative detection of mole
; FILE REFERENCE: 12671/1
; CURRENT APPLICATION NUMBER: US/10/331.109
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: PCT/EP01/07575
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 100 33 334.6
; PRIOR FILING DATE: 2000-07-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 21
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence:
US-10-331-109-21

Query Match
Best Local Similarity 69.3%; Score 10.4; DB 8; Length 16;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 UAACGUGAAG 15
1 :|||:|||||
Db 13 TAAGTGAAGAT 2

RESULT 9
US-09-846-903-24/c
; Sequence 24, Application US/09846903
; GENERAL INFORMATION:
; APPLICANT: Connor, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: 38-21(15678)B promoters
; CURRENT APPLICATION NUMBER: US/09/846.903
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 24
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fully
; OTHER INFORMATION: synthesized primer
US-09-846-903-24

Query Match
Best Local Similarity 83.3%; Score 10.4; DB 6; Length 17;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAUACGUGAAG 13
1 :|||:|||||

Db 16 GACACGTGAG 5

RESULT 10
US-10-310-188-80491/c
; Sequence 80491, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310.188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 80491
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-80491

Query Match
Best Local Similarity 75.0%; Score 10.4; DB 9; Length 17;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AUACGUGAAGA 14
1 :|||:|||||
Db 15 ATAACGTGAAAA 4

RESULT 11
PCT-US03-03662-97/c
; Sequence 97, Application PC/TUS0303662
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Mowlygen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Express
; FILE REFERENCE: 02-1005-A (400/083)
; CURRENT APPLICATION NUMBER: PCT/US03/03662
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: Patentln version 3.2
; SEQ ID NO 97
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sens
PCT-US03-03662-97

Query Match
Best Local Similarity 75.0%; Score 10.4; DB 1; Length 19;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 AUAACGUGAGA 14
1:1111111111
DB 12 ATACGCTGAGA 1

RESULT 12

PCT-US03-03662-336
; Sequence 336, Application PC/TUS0303662
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA interference mediated inhibition of Cyclin D1 Gene Expression
; FILE REFERENCE: 02-1005-A (400/083)
; CURRENT APPLICATION NUMBER: PCT/US03/03662
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 336
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense region
PCT-US03-03662-336

Query Match 69.3%; Score 10.4; DB 1; Length 19;

Best Local Similarity 91.7%; Pred. No. 6.2e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 AUAACGUGAGA 14
1111111111
DB 8 AUAACGUGAGA 19

RESULT 13

US-10-310-188-14089
; Sequence 14089, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14089
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-14089

Query Match 69.3%; Score 10.4; DB 9; Length 19;
Best Local Similarity 83.3%; Pred. No. 6.2e+04;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 2 GAUACGUGAG 13
1111111111
DB 8 GATACGGGAG 19

RESULT 14

PCT-US02-38806-82
; Sequence 82, Application PC/TUS0238806
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Therianos, Stavros
; APPLICANT: Coleman, Paul
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: MULTIPLEX REAL-TIME QUANTITATIVE PCR
; FILE REFERENCE: 21108.0009PI
; CURRENT APPLICATION NUMBER: PCT/US02/38806
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/397,475
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/336,095
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /note =
PCT-US02-38806-82

Query Match 69.3%; Score 10.4; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 6.2e+04;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 AUAACGUGAGA 14
1111111111
DB 8 ACACGCTGAGA 19

RESULT 15

US-10-317-277A-73/C
; Sequence 73, Application US/10317277A
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
; FILE REFERENCE: RTS-0473
; CURRENT APPLICATION NUMBER: US/10/317,277A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-317-277A-73

Query Match 69.3%; Score 10.4; DB 8; Length 20;

Best Local Similarity 75.0%; Pred. No. 6.2e+04;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 AUAACGUGAGA 14
1111111111
DB 20 ATACGCTGAGA 9

Search completed: May 22, 2003, 21:35:56
Job time : 374.364 secs

GenCore version 5.1.4-p5-4578
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 16:53:27 ; Search time 1045.64 Seconds

(Without alignments)
500.987 Million cell updates/sec

Title: US-09-780-929-98

Perfect score: 18

Sequence: 1 aauggcuaucgugcga 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 332216

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_ov:*
- 5: gb_ov:*
- 6: gb_ov:*
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- 8: gb_ov:*
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- 41: gb_ov:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	AX214296
2	12.8	71.1	20	6	AX295903
3	12.2	67.8	20	6	AX293899
4	11.8	65.6	20	6	AX293092
5	11.8	65.6	20	6	E30812
6	11.4	63.3	17	6	AR057682
7	11.4	63.3	17	6	AR057773
8	11.4	63.3	17	6	AR115440
9	11.4	63.3	17	6	AR115531
10	11.2	62.2	17	6	AX010333
11	11.2	62.2	17	6	AX215191
12	11.2	62.2	17	6	105557
13	10.8	60.0	20	6	AX293459
14	10.6	58.9	18	6	AX189338
15	10.6	58.9	20	6	AR063454
16	10.6	58.9	20	6	AX293222
17	10.4	57.8	15	6	AR033731
18	10.4	57.8	15	6	AR113553
19	10.4	57.8	15	6	157960
20	10.4	57.8	20	6	AX293280
21	10.4	57.8	20	6	AX294297
22	10.2	56.7	15	6	AR120152
23	10.2	56.7	17	6	AR190327
24	10.2	56.7	17	6	AR190328
25	10.2	56.7	17	6	AR190329
26	10.2	56.7	17	6	AX216858
27	10.2	56.7	17	6	AX217220
28	10.2	56.7	18	6	AR081732
29	10.2	56.7	19	6	109664
30	10.2	56.7	20	6	A79710
31	10.2	56.7	20	6	AX293581
32	10.2	56.7	20	6	AX295607
33	10.2	56.7	20	6	AX452366
34	10.2	56.7	20	6	E43264
35	10.2	56.7	20	6	E43283
36	10.2	56.7	12	6	A92476
37	10	55.6	12	6	AR106027
38	10	55.6	18	6	AX467000
39	10	55.6	20	6	AX278397
40	10	55.6	20	6	AX278439
41	10	55.6	20	6	AX294871
42	10	55.6	20	6	AX319927
43	10	55.6	20	6	131196
44	9.8	54.4	16	6	AR105448
45	9.8	54.4	17	6	AR190326

ALIGNMENTS

RESULT 1
AX214296
LOCUS AX214296
DEFINITION Sequence 109 from Patent WO0159102.
ACCESSION AX214296
VERSION AX214296.1 GI:15524373
KEYWORDS
ORGANISM
SOURCE
synthetic construct.
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Breaker, R. and Emilsson, G.
TITLE Nucleozymes with endonuclease activity
PATENT: WO 0159102-A 109 16-AUG-2001;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Yale University (US)

ORIGIN

CC Strandedness: Single;

ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 20;
Best Local Similarity 60.0%; Pred. No. 9.2e+04;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 UGCCUUAUCGGUGC 17
Db 20 TGCTCTCTCGGTGC 6

RESULT 6
LOCUS AR057682 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1886 from patent US 5837542.
ACCESSION AR057682
VERSION AR057682.1 GI:5983259
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwigen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1886 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"

BASE COUNT 1 a 5 c 7 g 4 t
ORIGIN

Query Match 63.3%; Score 11.4; DB 6; Length 17;
Best Local Similarity 69.2%; Pred. No. 1.5e+05;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGCCTGTCTCGGTGC 16
Db 2 GGCCTGTCTCGGTGC 14

RESULT 7
LOCUS AR057773 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1977 from patent US 5837542.
ACCESSION AR057773
VERSION AR057773.1 GI:5983350
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwigen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1977 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"

BASE COUNT 1 a 5 c 7 g 4 t
ORIGIN

Query Match 63.3%; Score 11.4; DB 6; Length 17;
Best Local Similarity 69.2%; Pred. No. 1.5e+05;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGCCTGTCTCGGTGC 16
Db 2 GGCCTGTCTCGGTGC 14

RESULT 8
LOCUS AR115440 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1886 from patent US 6132967.
ACCESSION AR115440
VERSION AR115440.1 GI:14095762
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwigen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
JOURNAL Intercellular adhesion molecule-1 (ICAM-1)
FEATURES Patent: US 6132967-A 1886 17-OCT-2000;
source 1..17
/organism="unknown"

BASE COUNT 1 a 5 c 7 g 4 t
ORIGIN

Query Match 63.3%; Score 11.4; DB 6; Length 17;
Best Local Similarity 69.2%; Pred. No. 1.5e+05;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGCCTGTCTCGGTGC 16
Db 2 GGCCTGTCTCGGTGC 14

RESULT 10
LOCUS AX010333 17 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 4 from Patent W09560007.
ACCESSION AX010333

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VERSION      AX010333.1  GI:9997186
KEYWORDS     Bacteriophage M13mp18.
SOURCE       Bacteriophage M13mp18
ORGANISM     Viruses.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Hamilton,A.L., Shchepinov,M.S., Southern,E.M., Elder,J.K. and
              Housby,J.N.
TITLE        Reagent and method
JOURNAL      Patent: WO 9960007-A 4 25-NOV-1999;
              HAMILTON ALAN LEWIS (GB); SHCHEPINOV MIKHAIL SPRGEVICH (GB);
              SOUTHERN EDWIN MELLOR (GB); ISTS INNOVATION (GB); ELDER JOHN
              KENNETH (GB); HOUSBY JOHN NICHOLAS (GB)
FEATURES     source
              1. .17
              /organism="Bacteriophage M13mp18"
              /db_xref="taxon:28360"
              /note="M13mp18 ssDNA"
BASE COUNT   3 a      3 c      9 g      2 t
ORIGIN
Query Match  62.2%; Score 11.2; DB 6; Length 17;
Best Local Similarity 68.8%; Pred. No. 2e+05;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY           2 AUGGCCUUAUCGGUGCG 17
             1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
             1 AAGGGCGATCGGTGCG 16

RESULT 11
LOCUS        AX215191      17 bp      mRNA      linear      PAT 07-SEP-2001
DEFINITION   Sequence 633 from Patent WO0159103.
ACCESSION    AX215191
VERSION      AX215191.1  GI:15525234
KEYWORDS     synthetic construct.
              synthetic construct
              artificial sequences.
              1 (bases 1 to 17)
SOURCE       Blatt,L., Mcswigen,J. and Chowrira,B.M.
              Method and reagent for the modulation and diagnosis of cd20 and
              nogo gene expression
              Patent: WO 0159103-A 633 16-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
              Mcswigen, James (US); Chowrira, Bharat M. (US)
FEATURES     source
              1. .17
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Nucleic Acid"
BASE COUNT   7 a      3 c      3 g      4 t
ORIGIN
Query Match  62.2%; Score 11.2; DB 6; Length 17;
Best Local Similarity 56.2%; Pred. No. 2e+05;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY           1 AAGGCCUUAUCGGUGCG 16
             1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
             1 AATGATCTATCTGTGC 1

RESULT 12
LOCUS        I05557      17 bp      DNA      linear      PAT 02-DEC-1994
DEFINITION   Sequence 1 from Patent EP 0285123.
ACCESSION    I05557
VERSION      I05557.1  GI:590718
KEYWORDS     Unknown.
              ORGANISM     Unknown.

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REFERENCE    1 (bases 1 to 17)
AUTHORS      Lehtovaara,P., Knowles,J., Kolvula,A., Bamford,J. and
              Reinikainen,T.
TITLE        A method for complete mutagenesis of nucleic acids
JOURNAL      Patent: EP 0285123-A2 1 05-OCT-1988;
              Location/Qualifiers
FEATURES     source
              1. .17
              /organism="unknown"
BASE COUNT   3 a      3 c      9 g      2 t
ORIGIN
Query Match  62.2%; Score 11.2; DB 6; Length 17;
Best Local Similarity 68.8%; Pred. No. 2e+05;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY           2 AUGGCCUUAUCGGUGCG 17
             1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
             2 AAGGGCGATCGGTGCG 17

RESULT 13
LOCUS        AX293459      20 bp      DNA      linear      PAT 21-NOV-2001
DEFINITION   Sequence 5221 from Patent WO0179548.
ACCESSION    AX293459
VERSION      AX293459.1  GI:17055142
KEYWORDS     synthetic construct.
              synthetic construct
              artificial sequences.
              1
SOURCE       Barany,F., Ziryi,M., Gerry,N.P., Favis,R. and Kliman,R.
              Method of designing addressable array for detection of nucleic acid
              sequence differences using ligase detection reaction
              Patent: WO 0179548-A 5221 25-OCT-2001;
              CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES     source
              1. .20
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Hypothetical Probe Sequence"
BASE COUNT   3 a      6 c      6 g      5 t
ORIGIN
Query Match  60.0%; Score 10.8; DB 6; Length 20;
Best Local Similarity 71.4%; Pred. No. 3.4e+05;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY           2 AUGGCCUUAUCGGUGCG 15
             1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
             1 ACGGCTAACGGTG 14

RESULT 14
LOCUS        AX189338      18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION   Sequence 43 from Patent WO0148202.
ACCESSION    AX189338
VERSION      AX189338.1  GI:15142850
KEYWORDS     synthetic construct.
              synthetic construct
              artificial sequences.
              1 (bases 1 to 18)
SOURCE       Glover,D.M., Yamamoto,R. and Henderson,D.
              Mus101 and homologues thereof
              Patent: WO 0148202-A 43 05-JUL-2001;
              Cyclacel Limited (GB)
FEATURES     source
              1. .18
              /organism="synthetic construct"
              /db_xref="taxon:32630"

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 16:52:30 ; Search time 175.636 Seconds

(Without alignments)
230.795 Million cell updates/sec

Title: US-09-780-929-98

Sequence: 18
1 aaugcccaucgugcgca 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 1367302

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_101002:*

- 1: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
- 2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
- 5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
- 6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
- 7: /SID2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
- 8: /SID2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
- 9: /SID2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
- 10: /SID2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
- 11: /SID2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
- 12: /SID2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
- 13: /SID2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
- 14: /SID2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
- 15: /SID2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
- 16: /SID2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
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- 18: /SID2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
- 19: /SID2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
- 24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	22	AA512348
2	12.8	71.1	20	24	AB195945
3	12.2	67.8	20	24	AB193941
4	11.8	65.6	20	20	AA94010
5	11.8	65.6	20	21	AA244197
6	11.8	65.6	20	24	AB193134
7	11.4	63.3	17	16	AA753656
8	11.4	63.3	17	16	AA753740
9	11.2	62.2	17	21	AA702004

10	11.2	62.2	17	21	AA239793
11	11.2	62.2	17	23	ABK00633
12	10.8	60.0	20	24	AB193501
13	10.6	58.9	18	22	ABD08688
14	10.6	58.9	18	24	ABL41065
15	10.6	58.9	20	20	AAV71835
16	10.6	58.9	20	24	AB193264
17	10.4	57.8	15	21	AA262886
18	10.4	57.8	20	24	ABN74903
19	10.4	57.8	20	24	AB193332
20	10.4	57.8	20	24	AB194339
21	10.2	56.7	15	19	AAV22883
22	10.2	56.7	15	22	AAV22883
23	10.2	56.7	17	18	AAV73065
24	10.2	56.7	17	18	AAV73066
25	10.2	56.7	17	18	AAV73067
26	10.2	56.7	17	23	ABK02300
27	10.2	56.7	17	23	ABK02662
28	10.2	56.7	18	20	AAV05734
29	10.2	56.7	18	23	AAV05734
30	10.2	56.7	18	23	AAV05734
31	10.2	56.7	19	11	AAV03309
32	10.2	56.7	20	18	AAV6749
33	10.2	56.7	20	20	AAV05983
34	10.2	56.7	20	20	AAV03160
35	10.2	56.7	20	21	AAV59788
36	10.2	56.7	20	22	AAV20507
37	10.2	56.7	20	22	AAV41780
38	10.2	56.7	20	24	AB193623
39	10.2	56.7	20	24	AB195649
40	10.2	56.7	20	24	AB142966
41	10	55.6	12	19	AAV44706
42	10	55.6	15	24	AAV16371
43	10	55.6	20	16	AAV05855
44	10	55.6	20	18	AAV5834
45	10	55.6	20	20	AAV04254

ALIGNMENTS

RESULT 1	AA512348	standard; DNA; 18 BP.
XX	AA512348;	
AC	21-NOV-2001	(first entry)
DT		
XX		
DE	DNA encoding deoxyribozyme #8.	
XX		
KW	Deoxyribozyme; cytosolic; endonuclease; RNA cleavage; DNA cleavage;	
KW	gene therapy; plant; fungus; bacteria; mammal; ribozyme; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200159102-A2.	
XX	16-AUG-2001.	
PD		
XX		
PF	08-FEB-2001; 2001WO-US04223.	
XX		
PR	08-FEB-2000; 2000US-0181360.	
XX	31-MAR-2000; 2000US-0193646.	
PA	(RIBO-) RIBOZYME PHARM INC.	
XX	(UTYA) UNITV YALE.	
XX		
PI	Breaker R, Belgelman L, Emilsson G;	
XX		
DR	WPI; 2001-536526/59.	
XX		
PT	New nucleic acids with endonuclease activity, such as ribozymes and	

M13mp18 ssDNA amp1
Human NCO Hammerhead
Capture oligonucleotide
Drosophila msl101
16s rRNA encoding
Bunchy top banana
Capture oligonucleotide
Substrate for HH r
Mouse caspase 2 an
Capture oligonucleotide
Mutant probe 3 use
Probe #4. Unident
Mouse flk-1 VEGF r
Mouse flk-1 VEGF r
Human NCO DNAzyme
Human NCO Amperly
primer for detecti
Otoferlin exon PCR
Bovine leukocyte a
Antisense oligonuc
Alternate primer 2
PCR primer used to
PCR primer for insu
Human MTHFR antise
Insulin receptor 9
Capture oligonucle
Capture oligonucle
Human chromosome 1
S. avidin11 Strept
ASO probe #7 for d
Primer A (Group 1)
Primer #1 to ampli
PCR primer used to

CC	Cytotoxic agents e.g. Cryptococcus neoformans, Candida albicans and
CC	Infectious agents e.g. Herpesvirus, HIV-1, Cytomegalovirus, Epstein-Barr virus and Polio virus,
CC	and parasitic infectious agents
CC	selected from Onchocerca volvulus, Entamoeba histolytica and Dirofilaria immitis.
CC	The method is also useful for detecting genetic diseases such as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC	Detecting cancer involving oncogenes, tumour suppressor genes, or genes involved in DNA amplification, replication, recombination or repair, the
CC	cancer is specifically associated with a gene selected from BRCA1 gene, p53 gene, human papillomavirus types 16 and 18 and Liver cancers. The
CC	method is also used for environmental monitoring, forensics and the food and feed industry, detecting compounds scanning (using e.g. a scanning electron microscope and infrared microscope) the support at the
CC	particular sites and identifying if ligation of the oligonucleotide probe sets occurred and correlating (using a computer) identified ligation to a presence or absence of the target nucleotide sequences. AB182074 to
CC	AB197546 represent oligonucleotide sequences used in the exemplification of the present invention.
XX	
SO	Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 other;
Query Match	71.1%; Score 12.8; DB 24; Length 20;
Best Local Similarity	68.8%; Pred. No. 7.2e+02;
Matches 11; Conservative	3; Mismatches 2; Indels 0; Gaps 0
OY	2 AUGGCCUACGGGCGC 17 1 111 :111111111
Db	2 ACGGCTTATCGGTGCG 17
RESULT 3	
AB193941	
ID	AB193941 standard; DNA; 20 BP.
XX	
XX	AB193941;
DT	16-FEB-2002 (first entry)
DE	Capture oligonucleotide Zip ID#1028 Oligo #9.
KW	Human; K-Ras; PCR primer; probe; capture probe; mutation detection; ligase detection reaction; LDR; p53; BRCA1; BRCA2; Infectious disease; infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer; oncogene; tumour suppressor; human papillomavirus; forensic; environmental monitoring; food industry; feed industry; ss.
OS	Synthetic.
PN	WO200179548-A2.
PD	25-OCT-2001.
PE	04-APR-2001; 2001WO-US10958.
PR	14-APR-2000; 2000US-197271P.
PA	(CORR) CORNELL RES FOUND INC.
PI	Barany F., Zivvi M., Gerry NP, Favis R, Kliman R;
WI	WPI; 2002-034366/04.
PT	Designing capture oligonucleotide probes for use on a support to which complementary oligonucleotides hybridize with little mismatch -
PS	Example 5; Fig 29; 300pp; English.
XX	
XX	The present invention describes a method (M1) for designing capture oligonucleotide probes (I) for use on a support to which complementary oligonucleotide probes (II) will hybridise with little mismatch, where (I) have melting temperatures within a narrow range. The method is useful for detecting infectious diseases caused by bacterial infectious agents e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal

CC Infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medineis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.

CC XX Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 other;

Query Match 67.8%; Score 12.2; DB 24; Length 20;

Best Local Similarity 64.7%; Pred. No. 1.6e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 AUGGCCUAGCGGCGA 18
Db 3 ATGACCAATCGATCGCA 19

RESULT 4

AAK94010/C
ID AAK94010 standard; DNA: 20 BP.

AAK94010;

13-SEP-1999 (first entry)

PCR primer used to amplify an ORF of Chlamydia pneumoniae.

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;

XX vaccine; neutralising epitope; PCR primer; ss.

OS Synthetic.

XX Chlamydia pneumoniae.

PN MO9927105-A2.

PD 03-JUN-1999.

XX 20-NOV-1998; 98MO-IB01890.

PR 04-NOV-1998; 98US-0107078.

XX 21-NOV-1997; 97FR-0014673.

PA (GEST) GENSET.

XX Griffais R;

PI WPI; 1999-357842/30.

DR WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae

XX Page 1636; Disclosure: 1912pp; English.

CC AAK91991-X97517 represent PCR primers used to amplify open reading

CC frames and other nucleic acid sequences from the genome of

CC Chlamydia pneumoniae (see AAK91990). C. pneumoniae causes respiratory

CC disease such as pneumonia and bronchitis and is thought to be a

CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent

CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded

CC by the open reading frames of the C. pneumoniae genome (see AAY34584-

CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC containing C. pneumoniae nucleotide sequences can also be used as
CC immunogenic compositions, especially where the vector directs the
CC expression of a neutralising epitope of C. pneumoniae.

XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other;

Query Match 65.6%; Score 11.8; DB 20; Length 20;

Best Local Similarity 66.7%; Pred. No. 2.8e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AUGGCCUAGCGGUG 15
Db 20 AATGCCCTACGATG 6

RESULT 5

AAZ44197/C
ID AAZ44197 standard; DNA: 20 BP.

AAZ44197;

24-MAR-2000 (first entry)

Murine cerebral nerve tissue differentiation DNA primer SAL.

Cerebral nerve tissue differentiation; murine; treatment; primer;

KW cerebral nerve disease; ss.

XX Mus sp.

PN JP11318468-A.

PD 24-NOV-1999.

XX 15-MAY-1998; 98JP-0152027.

PR 15-MAY-1998; 98JP-0152027.

XX (KANA-) ZH KANAGAWA KAGAKU GIYUTSU ACAD.

PA (MEIR) MEIRI MILK PROD CO LTD.

XX WPI; 2000-090527/08.

PT A new protein participating in the differentiation of cerebral nerve

XX tissue cell - for the prevention and treatment of cerebral nerve tissue

XX Example 4; Page 13; 22pp; Japanese.

CC This invention describes a novel murine protein which is capable of

CC inducing the differentiation of cerebral nerve tissue. The protein and

CC the gene are expected to be used for the prevention and the treatment

CC of cerebral nerve diseases. AAZ44193-244202 represent primers used in

CC the isolation of the cerebral nerve tissue differentiation associated

CC protein described in the method of the invention.

XX Sequence 20 BP; 7 A; 7 C; 4 G; 2 T; 0 other;

Query Match 65.6%; Score 11.8; DB 21; Length 20;

Best Local Similarity 60.0%; Pred. No. 2.8e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 UGCGCCUAGCGGUGCG 17
Db 20 TGGTCTCTCGTGG 6

RESULT 6

AB193134

ID AB193134 standard; DNA: 20 BP.

XX AB193134;

XX

DT 15-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide zip ID#221 oligo #9.
 XX
 KM Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KM lligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
 KM cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
 KM environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO2001/9548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US10958.
 XX
 PR 14-APR-2000; 2000US-197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch -
 XX
 PS Example 5; Fig 29; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Diacnulus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving Oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention.
 CC
 XX
 SQ Sequence 20 BP; 1 A; 6 C; 6 G; 7 T; 0 other;
 XX
 Query Match 65.6%; Score 11.8; DB 24; Length 20;
 Best Local Similarity 60.0%; Pred. No. 2.8e+03;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 OY 3 UGCGCUAUCGUGCG 17
 : ||:|:| |:
 Db 6 TGCCCTATCTGTGCG 20

RESULT 7
 AAT53656
 ID AAT53656 standard; RNA; 17 BP.
 XX
 AC AAT53656;
 XX

DT 27-MAR-1997 (first entry)
 XX
 DE Rat ICAM hammerhead ribozyme target sequence (nt. position 2341).
 XX
 KM Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KM gene expression; downregulation; Interleukin-5; IL-5; ICAM-1;
 KM intercellular adhesion molecule; rel A; tumour necrosis factor;
 KM TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KM translocation; chronic myelogenous leukemia; CML; cancer;
 KM Philadelphia chromosome; inflammation; autoimmune disease;
 KM atherosclerosis; myocardial infarction; stroke; restenosis;
 KM transplant rejection; rheumatoid arthritis; psoriasis;
 KM myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KM human immunodeficiency virus; acquired immune deficiency syndrome;
 KM AIDS; ss.
 XX
 OS Rattus rattus.
 XX
 PN WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-IB00156.
 XX
 PR 30-JAN-1995; 95US-0380734.
 PR 23-FEB-1994; 94US-0201109.
 PR 29-MAR-1994; 94US-0218934.
 PR 04-APR-1994; 94US-0222795.
 PR 07-APR-1994; 94US-0224483.
 PR 15-APR-1994; 94US-0227958.
 PR 15-APR-1994; 94US-0228041.
 PR 18-MAY-1994; 94US-0245736.
 PR 06-JUL-1994; 94US-0271280.
 PR 15-AUG-1994; 94US-0291932.
 PR 16-AUG-1994; 94US-0291433.
 PR 17-AUG-1994; 94US-0292620.
 PR 19-AUG-1994; 94US-0293520.
 PR 02-SEP-1994; 94US-0300000.
 PR 08-SEP-1994; 94US-0303039.
 PR 23-SEP-1994; 94US-0311486.
 PR 23-SEP-1994; 94US-0311749.
 PR 28-SEP-1994; 94US-0314397.
 PR 03-OCT-1994; 94US-0316771.
 PR 07-OCT-1994; 94US-0319492.
 PR 11-OCT-1994; 94US-0321993.
 PR 04-NOV-1994; 94US-0334847.
 PR 10-NOV-1994; 94US-0337608.
 PR 28-NOV-1994; 94US-0345516.
 PR 16-DEC-1994; 94US-0357577.
 PR 23-DEC-1994; 94US-0363233.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpelsky A, Kisich K, Matulic-Adamic J;
 PI McSwiggan JA, Modak A, Pavco P, Beigelman L, Sullivan SM,
 PI Sweedler D, Thompson JD, Tracz D, Usman N, Wincott FE,
 PI Woolf T;
 XX
 DR WPI; 1995-351090/45.
 XX
 PT Ribozymes having modified bases and methods for producing them
 PT for use in inhibiting disease related genes
 XX
 PS Claim 2; Page 203; 407pp; English.
 XX
 CC The present sequence represents a preferred target sequence for
 CC an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1
 CC mRNA at the nucleotide base position indicated in the DE line.
 CC Regions of the mRNA that do not form secondary folding
 CC structures and that contain potential hammerhead and hairpin
 CC ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and

CC synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and
 CC thereby inhibit ICAM-1 expression, making them useful for reducing
 CC transplant rejection and alleviating symptoms in patients with
 CC rheumatoid arthritis, asthma and other inflammatory disorders.

SO Sequence 17 BP; 1 A; 5 C; 7 G; 4 U; 0 other;

Query Match 63.3%; Score 11.4; DB 16; Length 17;
 Best Local Similarity 92.3%; Pred. No. 4.7e+03;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 GGCCUACGCGUC 16
 Db 2 GGCCUGCGCGUC 14

RESULT 8
 AAT53740
 ID AAT53740 standard; RNA; 17 BP.

XX AAT53740;

DT 03-APR-1997 (first entry)

DE Rat ICAM hammerhead ribozyme target sequence (nt. position 2872).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW Philadelphia chromosome; myelogenous leukemia; CML; cancer;
 KW Philadelphia chromosome; myelogenous leukemia; CML; cancer;
 KW atherosclerosis; myocardial infarction; autoimmune disease;
 KW transplant rejection; rheumatoid arthritis; psoriasis; HIV;
 KW myocardial ischemia; Kawasaki disease; septic shock; HTV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome;
 KW AIDS; ss.

XX Rattus rattus.

XX WO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB00156.

XX 30-JAN-1995; 95US-0380734.

XX 23-FEB-1994; 94US-0201109.

XX 29-MAR-1994; 94US-0218934.

XX 04-APR-1994; 94US-0222795.

XX 07-APR-1994; 94US-0224483.

XX 15-APR-1994; 94US-0227958.

XX 15-APR-1994; 94US-0228041.

XX 18-MAY-1994; 94US-0245736.

XX 06-JUL-1994; 94US-0271280.

XX 15-AUG-1994; 94US-0291932.

XX 16-AUG-1994; 94US-0291433.

XX 17-AUG-1994; 94US-0292620.

XX 19-AUG-1994; 94US-0293520.

XX 02-SEP-1994; 94US-0300000.

XX 08-SEP-1994; 94US-0303039.

XX 23-SEP-1994; 94US-0311486.

XX 28-SEP-1994; 94US-0311749.

XX 03-OCT-1994; 94US-0316771.

XX 07-OCT-1994; 94US-0319492.

XX 11-OCT-1994; 94US-0321993.

XX 04-NOV-1994; 94US-0334847.

XX 10-NOV-1994; 94US-0337608.

XX 28-NOV-1994; 94US-0345516.

XX 16-DEC-1994; 94US-0357577.

XX 23-DEC-1994; 94US-0363233.

XX (RIBO-) RIBOZYME PHARM INC.

PA Stinchcomb DT, Chowitra B, Dizenzo A, Draper KG, Dudycz LM;

PI Grimm S, Karpelsky A, Kisch K, Matulic-Adamic J;

PI McSwiggen JA, Modak A, Pavco P, Beigelman L, Sullivan SM;

PI Sweedler D, Thompson JD, Tracz D, Usman N, Wincott FE;

PI Woolf T;

XX WPI; 1995-351090/45.

XX Ribozyms having modified bases and methods for producing them

PT for use in inhibiting disease related genes

XX Claim 2; Page 204; 407pp; English.

XX The present sequence represents a preferred target sequence for

CC an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1

CC mRNA at the nucleotide base position indicated in the DE line.

CC Regions of the mRNA that do not form secondary folding

CC structures and that contain potential hammerhead and hairpin

CC ribozyme cleavage sites were identified by computer analysis.

CC Ribozymes directed against these mRNA sequences were designed and

CC synthesised with modifications that improve their nuclease

CC resistance. The ribozymes cleave the ICAM-1 target sequences and

CC thereby inhibit ICAM-1 expression, making them useful for reducing

CC transplant rejection and alleviating symptoms in patients with

CC rheumatoid arthritis, asthma and other inflammatory disorders.

XX Sequence 17 BP; 1 A; 5 C; 7 G; 4 U; 0 other;

SO Query Match 63.3%; Score 11.4; DB 16; Length 17;

Best Local Similarity 92.3%; Pred. No. 4.7e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCUACGCGUC 16

Db 2 GGCCUGCGCGUC 14

XX Rattus rattus.

XX WO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995; 95WO-IB00156.

XX 30-JAN-1995; 95US-0380734.

XX 23-FEB-1994; 94US-0201109.

XX 29-MAR-1994; 94US-0218934.

XX 04-APR-1994; 94US-0222795.

XX 07-APR-1994; 94US-0224483.

XX 15-APR-1994; 94US-0227958.

XX 15-APR-1994; 94US-0228041.

XX 18-MAY-1994; 94US-0245736.

XX 06-JUL-1994; 94US-0271280.

XX 15-AUG-1994; 94US-0291932.

XX 16-AUG-1994; 94US-0291433.

XX 17-AUG-1994; 94US-0292620.

XX 19-AUG-1994; 94US-0293520.

XX 02-SEP-1994; 94US-0300000.

XX 08-SEP-1994; 94US-0303039.

XX 23-SEP-1994; 94US-0311486.

XX 28-SEP-1994; 94US-0311749.

XX 03-OCT-1994; 94US-0316771.

XX 07-OCT-1994; 94US-0319492.

XX 11-OCT-1994; 94US-0321993.

XX 04-NOV-1994; 94US-0334847.

XX 10-NOV-1994; 94US-0337608.

XX 28-NOV-1994; 94US-0345516.

XX 16-DEC-1994; 94US-0357577.

XX 23-DEC-1994; 94US-0363233.

PS Claim 37: Page 62; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the T12 Orphan receptor, EAR3/COP-TF-1, the GATA
CC transcription factor gene, IRF-2 and/or the CAAT Displacement
CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.
XX
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 other;
XX
QY Query Match 62.2%; Score 11.2; DB 21; Length 17;
Best Local Similarity 62.5%; Pred. No. 6.1e+03;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
XX
Db 3 UGCGCCUAGCGGCGCA 18
16 TGGCCCAATAGGTGCCA 1
XX
RESULT 10
AAZ39793
ID AAZ39793 standard; DNA; 17 BP.
XX
AC AAZ39793;
XX
DT 06-MAR-2000 (first entry)
XX
DE M3mp18 ssDNA amplifying primer B1.
XX
KM Nucleic acid analysis; mass spectrometry; chemical compound analysis;
KM PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9960007-A2.
XX
PD 25-NOV-1999.
XX
PF 17-MAY-1999; 99WO-GB01561.
XX
PR 15-MAY-1998; 98EP-0303873.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Southern EM, Shephelov MS, Housby JN, Hamilton AL, Elder JK;
XX
DR WPI; 2000-062435/05.
XX
PT Analysis of compounds using a solid support, labeled compounds and mass
XX
PS spectrometry
XX
XX Example 3: Page 26; 65pp; English.
XX
CC The invention provides new methods for the analysis of compounds,
CC particularly nucleic acids, that use a solid support, labeled compounds
CC and mass spectrometry. A novel method of making a set of labeled
CC compounds, using of a support and a set of labels, comprises: (1) at
CC least one first or intermediate step comprising dividing the support into
CC lots, performing a different chemical reaction on each lot of the support
CC so as either to modify that lot of the support or to couple a chemical
CC moiety to that lot of the support, tagging a fraction of each lot of the
CC moiety with a different label, and combining the lots of the support,
CC and (2) at least one intermediate or final step comprising dividing the
CC support into lots, performing a different chemical reaction on each lot
CC of the support, so as either to modify that lot of the support or to
CC couple a chemical moiety to that lot of the support, tagging a fraction
CC of each lot of the support with a different label, where each different
CC label is linked to a chemical moiety a labeled compound which is
CC separable from the support, and combining the lots of the support. The
CC methods and products are used for the analysis of chemical compounds,

CC particularly nucleic acid molecules.
XX
SQ Sequence 17 BP; 3 A; 3 C; 9 G; 2 T; 0 other;
XX
QY Query Match 62.2%; Score 11.2; DB 21; Length 17;
Best Local Similarity 68.8%; Pred. No. 6.1e+03;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2 AUGGCCUAGCGGCGC 17
1 AAGGCGCATCGGTGCG 16
XX
Db 1 AAGGCGCATCGGTGCG 16
XX
RESULT 11
ABK00633/c
ID ABK00633 standard; RNA; 17 BP.
XX
AC ABK00633;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human NCOGO Hammerhead Ribozyme #633.
XX
KM Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KM cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KM muscular; CD20; neurite growth inhibitor gene; NCOGO; hammerhead ribozyme;
KM DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KM inflammatory arthropathy; central nervous system injury;
KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KM Parkinson's disease; ataxia; Huntington's disease;
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001MO-US04273.
XX
PR 11-FEB-2000; 2000US-181797P.
XX
PR 28-FEB-2000; 2000US-185516P.
XX
PR 06-MAR-2000; 2000US-187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, MCSwigen J, Chowrira BW;
XX
DR WPI; 2001-607195/69.
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX
PT constructs, which down regulate expression of a CD20 gene or neurite
XX
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
XX
PT and central nervous system injury
XX
PS Claim 88: Page 76; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NCOGO).
CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN
CC motif) pr an amberzyme (cleaving RNA with an NGN triplet), a zinzyme
CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used

CC to cleave RNA of CD20 in the presence of a divalent cation that is
CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
CC CD20 activity of the cell and treat a patient having a condition
CC associated with the level of CD20. The treatment may further comprise the
CC use of one or more therapies. In particular, the CD20 targeting
CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
CC thrombocytopenia, and inflammatory arthropathy. The NCOG-targeting
CC nucleic acid is used to cleave RNA of the NCOG gene in the presence of a
CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
CC may be contacted with a cell to reduce NCOG activity of the cell and
CC treat a patient having a condition associated with the level of NCOG. The
CC treatment may further comprise the use of one or more therapies.
CC In particular, the NCOG-targeting nucleic acid may be used to treat
CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NCOG expression. The
CC present sequence is a hammerhead ribozyme of the invention.

SO Sequence 17 BP; 7 A; 3 C; 3 G; 4 U; 0 other;

Query Match 62.2%; Score 11.2; DB 23; Length 17;
Best Local Similarity 56.2%; Pred. No. 6.1e+03;

Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 A AUGGCCUAGCGGUC 16
||| ||| ||| |||

Db 16 AATGATCTATCTGTGC 1

RESULT 12

AB193501
ID AB193501 standard; DNA; 20 BP.

AC AB193501;

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#588 oligo #9.

KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW lissase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.

OS Synthetic.

PN WO200179548-A2.

PD 25-OCT-2001.

PE 04-APR-2001; 2001WO-US10958.

PR 14-APR-2000; 2000US-197271P.

PA (CORR) CORNELL RES FOUND INC.

PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;

DR WPI; 2002-034366/04.

PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -

PS Example 5; Fig 29; 300pp; English.

CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents,
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.

SO Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 other;

Query Match 60.0%; Score 10.8; DB 24; Length 20;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;

Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 AUGGCCUAGCGGUG 15
||||| ||| |||

Db 1 ACGGCTTACCGGTG 14

RESULT 13

AAD08688/c
ID AAD08688 standard; DNA; 18 BP.

AC AAD08688;

DT 04-SEP-2001 (first entry)

DE Drosophila mus101 genomic and partial cDNA sequencing primer, GENY9P8.

KW Mus101; BRCA1 C-Terminus; BRCT; gene therapy; tumour; mitosis inhibitor;
KW DNA repair; cell cycle regulation; passive immunotherapy; primer; ss.

OS Drosophila sp.

PN WO200148202-A1.

PD 05-JUL-2001.

PE 21-DEC-2000; 2000WO-GB04956.

PR 24-DEC-1999; 99GB-0030708.

PA (CYCL-) CYCLACEL LTD.

PI Glover DM, Yamamoto R, Henderson D;

DR WPI; 2001-418282/44.

PT Novel mus101 polypeptide, a member of BRCT superfamily derived from
PT Drosophila useful for identifying substance capable of affecting mus101
PT function, and for treating tumor -

PS Example; Page 44; 108pp; English.

CC The present sequence is a primer which is used to sequence the
CC Drosophila mus101 genomic and partial cDNAs. The mus101 is a member of

CC BRCT (BRCA1 C-Terminus) superfamily. The mus101 polynucleotide probe is
 CC used for detecting the presence or absence of mus101 polynucleotide in a
 CC biological sample by bringing the biological sample containing DNA or
 CC RNA into contact with mus101 polynucleotide probe under hybridising
 CC conditions, and detecting any duplex formed between mus101 polynucleotide
 CC probe and mus101 polynucleotide in the sample. The mus101 and its
 CC polynucleotide are useful in gene therapy. The mus101 is useful for
 CC identifying a substance capable of affecting mus101 function, and the
 CC substance is useful for treating tumour, for inhibiting mitosis and for
 CC increasing the susceptibility of a tumour cell to a DNA damaging agent.
 CC The mus101 is also useful for identifying substances which affects DNA
 CC repair and cell cycle regulation, in vitro or in vivo cell culture system
 CC to study the role of mus101 and its homologues in disease, and as
 CC immunogens. The antibody to mus101 is useful in diagnosis and in passive
 CC immunotherapy. It is also useful for detecting mus101 in a biological
 CC sample.

XX Sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 other;

Query Match 58.9%; Score 10.6; DB 22; Length 18;

Best Local Similarity 58.8%; Pred. No. 1.4e+04;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 AUGCCCAUCCGUGCGA 18

Db 17 AAGCTTATGTCGCA 1

RESULT 14
 ABL41065/c
 ID ABL41065 standard; DNA; 18 BP.

XX ABL41065;

XX 12-AUG-2002 (first entry)

DE 16s rRNA encoding DNA specific probe.

KM Microbe; water treatment; 16s rRNA; probe; ss.

OS Synthetic.

PN JP2002101884-A.

XX 09-APR-2002.

PF 27-SEP-2000; 2000JP-0294854.

PR 27-SEP-2000; 2000JP-0294854.

PA (YAMA) NIPPON STEEL CORP.

XX WPI; 2002-440454/47.

PT Specifying microbes for evaluation and control of waste water treatment process -

PS Disclosure; Page 6; 11pp; Japanese.

XX The invention relates to specifying complex microbes as an index to
 CC evaluate a water treatment process. The method involves: (1) extracting
 CC microbial DNA which cannot be adapted; (2) amplifying partial regions of
 CC the microbial genes; (3) separating the aggregate of the resultant DNA
 CC fragments; and (4) using the DNA to compare the growing conditions of the
 CC microbes and conditions of the water treatment process. The present
 CC sequence represents a probe specific for a 16s rRNA encoding DNA,
 CC used in the course of the invention.

XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 other;

Query Match 58.9%; Score 10.6; DB 24; Length 18;
 Best Local Similarity 64.7%; Pred. No. 1.4e+04;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 AUGCCCAUCCGUGCGA 18
 Db 18 ATGGCTTATGTCGCA 2

RESULT 15

AAV71835
 ID AAV71835 standard; DNA; 20 BP.

XX AAV71835;

XX 10-FEB-1999 (first entry)

DE Bunchy top banana virus (BBTV) DNA specific primer BB-1.

KM Banana bunchy top virus; BBTV; PCR technique; plant; tissue; banana;
 KM Musa; phloem damage; aphid; nucleic acid detection; PCR primer; ss.

OS Synthetic.

PN US5846705-A.

XX 08-DEC-1998.

PF 06-APR-1995; 95US-0418071.

PR 06-APR-1995; 95US-0418071.

PA (BIOT-) DEV CENT BIOTECHNOLOGY.

PI Soong T, Wu R, You L;

XX WPI; 1999-059037/05.

PT Nucleic acids having banana bunchy top virus component sequences -
 PT used to design primers for use in polymerase chain reaction
 PT detection of the virus

PS Claim 10; Column 9; 27pp; English.

XX Sequences AAV71835 to AAV71841 represent PCR primers specific for the
 CC banana bunchy top virus (BBTV) DNA. The invention provides BBTV DNA I
 CC (clone 7-4-2) circular single stranded (css) DNA, CC and DNA II (clone
 CC 2-17) css DNA sequences (AAV71832 and AAV71833) and the proteins
 CC (AAW7439 and AAW87460) encoded by the open reading frames in the
 CC nucleotide sequences. The nucleic acid sequences (AAV71830 to AAV71833)
 CC are used as the basis for the construction of PCR primers, to detect BBTV
 CC infection. The PCR technique is used for detecting BBTV in plant tissues
 CC (preferably banana, especially Musa species). The virus, one of the most
 CC important banana species viruses, causes phloem damage and is transmitted
 CC by aphids. PCR detection gives accurate, reliable and specific
 CC determination of absence or presence of the virus.

XX Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 other;

Query Match 58.9%; Score 10.6; DB 20; Length 20;
 Best Local Similarity 58.8%; Pred. No. 1.4e+04;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 AUGCCCAUCCGUGCGA 18
 Db 2 ATGGCTTATGAGGCA 18

Search completed: May 22, 2003, 19:04:27
 Job time: 178.636 secs

GenCore version 5.1.4-p5.4578
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OW nucleic - nucleic search, using sw model

Run on: May 22, 2003, 18:32:43 ; Search time 1311.82 Seconds
(Without alignments)
222.225 Million cell updates/sec

Title: US-09-780-929-98

Sequence: 1 aauggcccaugugugcga 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 5800

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estlin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hlc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hlc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_man:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	9.6	53.3	20	17	AZ514794
C 2	9.2	51.1	20	17	AZ601483
C 3	8.4	46.7	15	14	BO511821
C 4	8.2	45.6	19	17	AZ329706
C 5	8.2	45.6	19	17	AZ515014
C 6	8.2	44.4	20	12	BF966452

RESULT 1	AZ514794/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
C 7	7.8	43.3	12	14	BO750930								
C 8	7.8	43.3	18	13	BM396285								
C 9	7.8	43.3	19	17	AZ787588								
C 10	7.8	43.3	19	17	AZ800646								
C 11	7.8	43.3	20	17	AZ779244								
C 12	7.8	43.3	20	17	BSMC21G06								
C 13	7.6	42.2	18	13	BM394638								
C 14	7.6	42.2	19	9	AA885697								
C 15	7.6	42.2	19	9	AA885697								
C 16	7.6	42.2	19	9	AA885697								
C 17	7.6	42.2	19	17	AZ696420								
C 18	7.6	42.2	19	17	AZ686832								
C 19	7.6	42.2	19	17	AZ936396								
C 20	7.4	41.1	20	17	AZ603553								
C 21	7.4	41.1	16	14	BO789979								
C 22	7.4	41.1	18	2	BSM007922								
C 23	7.4	41.1	19	2	BSM007922								
C 24	7.4	41.1	19	17	AZ429998								
C 25	7.4	41.1	19	17	AZ814112								
C 26	7.2	40.0	18	2	BSM007922								
C 27	7.2	40.0	19	17	AZ426075								
C 28	7.2	40.0	19	17	AZ785324								
C 29	7.2	40.0	19	17	AZ786704								
C 30	7.2	40.0	19	17	AZ954781								
C 31	7.2	40.0	20	2	BSM008058								
C 32	7.2	40.0	20	17	AZ600911								
C 33	7.2	40.0	20	17	AZ603262								
C 34	7.2	40.0	20	17	AZ776456								
C 35	7.2	40.0	20	17	AZ782314								
C 36	7.2	40.0	20	17	AZ938837								
C 37	7.2	38.9	15	10	AZ247980								
C 38	7.2	38.9	15	13	BM400409								
C 39	7.2	38.9	15	14	RA1075								
C 40	7.2	38.9	17	14	BO605828								
C 41	7.2	38.9	19	9	AI641650								
C 42	7.2	38.9	19	17	AZ303767								
C 43	7.2	38.9	19	17	AZ358825								
C 44	7.2	38.9	19	17	AZ480102								
C 45	7.2	38.9	19	17	AZ514722								

ALIGNMENTS

RESULT 1
AZ514794/c 20 bp DNA linear GSS 05-OCT-2000
1M0361C13R Mouse 10kb plasmid UGCCIM library Mus musculus genomic
clone UGCCIM0361C13 R, DNA sequence.
AZ514794
AZ514794.1 GI:10696110
GSS.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10Kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84117, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0361 row: C column: 13
 Seq primer: CACACAGCAACAGCTATACCC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20

source
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0361C13"
 /clone_lib="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 4 a
 6 c 7 g 3 t

Query Match 53.3%; Score 9.6; DB 17; Length 20;
 Best Local Similarity 56.2%; Pred. No. 6.6e+05;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 AUGGCCUAGCGUGCG 17
 1:|||||:11:11
 Db 17 ATGGCCACTGTGCTGC 2

RESULT 2
 A2601483/c 20 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0419H15R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 DEFINITION clone UUCG1M0419H15 R, DNA sequence.
 ACCESSION A2601483
 VERSION A2601483.1 GI:11723673
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00

Plate: 0419 row: H column: 15
 Seq primer: CACACAGCAACAGCTATACCC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20

source
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0419H15"
 /clone_lib="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 3 a
 6 c 7 g 4 t

Query Match 51.1%; Score 9.2; DB 17; Length 20;
 Best Local Similarity 64.3%; Pred. No. 1e+06;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 UGGCCUAGCGUGCG 16
 1:|||||11:111
 Db 19 TGGCCACTGTGC 6

RESULT 3
 B0511821 15 bp mRNA linear EST 10-JUN-2002
 LOCUS EST619236 Generation of a set of potato cDNA clones for microarray
 DEFINITION analyses mixed potato tissues Solanum tuberosum cDNA clone STMH018
 5' end, mRNA sequence.
 ACCESSION B0511821
 VERSION B0511821.1 GI:21370690
 KEYWORDS EST.
 SOURCE potato.
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 15)
 Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,M., Smart,C., Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and Karamecheva,S.A.
 Generation of a set of potato cDNA clones for microarray analyses
 Unpublished (2002)
 Other-ESTs: EST619237
 CONTACT: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Email: potatodtgr.org
 This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or cdna@resgen.com
 Seq primer: T3.

FEATURES
source

Location/Qualifiers

1. 15
/organism="Solanum tuberosum"
/cultivar="Kennebec Or Bintje"
/db_xref="taxon:4113"
/clone="STMH018"
/clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Combination of untreated and phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."
BASE COUNT
ORIGIN

Query Match 46.7%; Score 8.4; DB 14; Length 15;
Best Local Similarity 60.0%; Pred.No. 2.3e+06;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAUGGCCUAD 10
|||||:
DB 5 AATGGCCTCT 14

RESULT 4
AZ329706/c

LOCUS 19 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0054D06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0054D06 R, DNA sequence.

ACCESSION AZ329706
VERSION AZ329706.1 GI:10390686
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0054 row: D column: 06

Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers

1. 19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0054D06"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

BASE COUNT
ORIGIN

Query Match 45.6%; Score 8.2; DB 17; Length 19;
Best Local Similarity 61.5%; Pred.No. 3.1e+06;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 GGCCUACGCGUC 16
|||||:
DB 17 GGCAATATAGGGGC 5

RESULT 5
AZ515014/c

LOCUS 19 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0054D06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0054D06 F, DNA sequence.

ACCESSION AZ515014
VERSION AZ515014.1 GI:10696330
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0054 row: D column: 06

Seq primer: CGTGTAAACGACGGCCACT
Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers

1. 19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0054D06"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321149b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT
ORIGIN

5 a 7 c 2 g 5 t

Query Match 45.6%; Score 8.2; DB 17; Length 19;
Best Local Similarity 61.5%; Pred. No. 3.1e+06;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 GGCCUACGGGCG 16
|||:|:|:|:|:
Db 17 GGCAATAGGCGC 5

RESULT 6
BF966452
LOCUS

DEFINITION 20 bp mRNA linear EST 23-JAN-2001
602287066F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:4375648 5',
mRNA sequence.

ACCESSION BF966452 GI:12386052
VERSION BF966452.2
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 20)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jan 16, 2001 this sequence version replaced g1:12333667.

Contact: Robert Strausberg, Ph.D.
Email: cgaups-femail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraiki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: ILM10041 row: d column: 17
High quality sequence stop: 20.

FEATURES
source

1..20
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4375648"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgaag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

BASE COUNT 3 a 5 c 10 g 2 t
ORIGIN

Query Match 44.4%; Score 8; DB 12; Length 20;
Best Local Similarity 75.0%; Pred. No. 3.9e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 UCGGUGCG 17
:|:|:|:|:|:
Db 8 TCGGTGCG 15

RESULT 7
BO750930/c 12 bp mRNA linear EST 18-JUL-2002
LOCUS EST631493 DSCIT Colletotrichum trifolii CDNA clone pDSCIT-51, mRNA
DEFINITION sequence.

ACCESSION BO750930
VERSION BO750930.1 GI:21906335
KEYWORDS EST.
SOURCE Colletotrichum trifolii.
ORGANISM Colletotrichum trifolii.

REFERENCE Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T.,
AUTHORS Cheung,F. and Fraser,C.M.
TITLE ESTs from mycelia of Colletotrichum trifolii race 1
JOURNAL Unpublished (2002)
COMMENT Other ESTs: EST631492

Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@pnuc101.crl.umn.edu
TIGR sequence name: MTSAA51TV More information is available at:
www.medicago.org

Seq primer: (gta ata cga ctc act ata ggg c).
Location/Qualifiers
1..12
/organism="Colletotrichum trifolii"
/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSCIT-51"
/clone_lib="DSCIT"
/tissue_type="mycelia"
/dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="DH5alpha"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: EcoRI; Isolator: 2SP2; CDNA was prepared from polyA+ enriched RNA. The CDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce *E. coli* Y1090 and phage DNA was purified from a liquid lysate. The CDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform *E. coli* DH5alpha which were plated onto medium with X-gal for selection of recombinants."

FEATURES
source

1..12
/organism="Colletotrichum trifolii"
/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSCIT-51"
/clone_lib="DSCIT"
/tissue_type="mycelia"
/dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
/lab_host="DH5alpha"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: EcoRI; Isolator: 2SP2; CDNA was prepared from polyA+ enriched RNA. The CDNA was ligated into Lambda gtl1 from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce *E. coli* Y1090 and phage DNA was purified from a liquid lysate. The CDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform *E. coli* DH5alpha which were plated onto medium with X-gal for selection of recombinants."

BASE COUNT 5 a 3 c 4 g 0 t
ORIGIN

Query Match 43.3%; Score 7.8; DB 14; Length 12;
Best Local Similarity 54.5%; Pred. No. 4.3e+06;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGCCUACGGU 14
|||:|:|:|:|:

Db 12 GGCTTCCTT 2

RESULT 8
LOCUS BM396285
DEFINITION BM396285 18 bp mRNA linear EST 17-JAN-2002
5009-0-2-A10.t.1 Chlcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM396285
VERSION BM396285.1 GI:18196338
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 18)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
J. and Klobutcher, L.,
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
CONTACT: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
SOURCE
1. 18
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chlcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK⁺. Details on library
preparation can be found in Chlcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 3 a 3 c 8 g 4 t
ORIGIN

Query Match 43.3%; Score 7.8; DB 13; Length 18;
Best Local Similarity 54.5%; Pred. No. 4.8e+06;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 UGCGCUAUGCG 13
|||||:|:|
Db 8 TGGCTTATCGG 18

RESULT 9
LOCUS A2787588 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0034A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0034A07 F, DNA sequence.

ACCESSION A2787588
VERSION A2787588.1 GI:12926529
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

JOURNAL COMMENT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0034 Row: A Column: 07
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
SOURCE
1. 19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC2M0034A07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (91147311419b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 10 a 3 c 5 g 1 t
ORIGIN

Query Match 43.3%; Score 7.8; DB 17; Length 19;
Best Local Similarity 54.5%; Pred. No. 4.8e+06;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGCCUAGCGU 14
|||||:|:|
Db 17 GGCTATTGT 7

RESULT 10
LOCUS A2800646 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0058H14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0058H14 R, DNA sequence.

ACCESSION A2800646
VERSION A2800646.1 GI:12952969
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

JOURNAL COMMENT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0038 row: H column: 14
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19

source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C2M0058H14"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 3 a 4 c 7 g 5 t
ORIGIN

Query Match 43.3%; Score 7.8; DB 17; Length 19;
Best Local Similarity 63.6%; Pred. No. 4.8e+06;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 4 GGCCUAGCGU 14
Db 5 GGCCCATTTGGT 15

RESULT 11
A2779244/c 20 bp DNA linear GSS 16-FEB-2001
LOCUS 2M001J11F Mouse 10kb plasmid U08C1M library Mus musculus genomic
DEFINITION A2779244
ACCESSION A2779244
VERSION A2779244.1 GI:12909701
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, R., Meenen, E., Petersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0015 row: I column: 19
Seq primer: CGTTGTAACAGCAGCCGACGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20

source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C2M0015119"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 9 a 3 c 6 g 2 t
ORIGIN

Query Match 43.3%; Score 7.8; DB 17; Length 20;
Best Local Similarity 54.5%; Pred. No. 4.9e+06;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAGCCUAGC 11
Db 18 AGTGTCTCTATC 8

RESULT 12
HSMC21G06 20 bp DNA linear GSS 29-MAY-1997
LOCUS HSMC21G06
DEFINITION H.sapiens DNA for trapped exon (ID HMC21G06), genomic survey
ACCESSION X88286
VERSION X88286.1 GI:1437772
KEYWORDS GSS.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 20)
Chen, H.M., Rossier, C., Christ, R. and Antonarakis, S.E.
Cloning of trapped exons from human chromosome 21
Unpublished
2 (bases 1 to 20)
Antonarakis, S.E.
Direct Submission
Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of Medical Genetics, University and Cantonal Hospital of Geneva, CMU, 1 rue Michel-Servet, 1211 Geneva, SWITZERLAND
3 (bases 1 to 20)
Chen, H., Christ, R., Rossier, C., Morris, M.A., Lalloi, M.D. and

Antonarakis, S.E.
Cloning of 559 potential exons of genes of human chromosome 21 by
exon trapping
JOURNAL Genome Res. 6 (8), 747-760 (1996)
MEDLINE 97011340
PUBMED 8858350

FEATURES
SOURCE Location/Qualifiers
1..20 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
1..20 /note="trapped exon"
5 a 5 c 5 g 4 t 1 others

BASE COUNT
ORIGIN

Query Match 43.3% Score 7.8; DB 17; Length 20;
Best Local Similarity 58.3%; Pred. No. 4.9e+06;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 CUAGCGUGCGA 18
1:1 1:1 1:1 1:1
Db 4 CTACCGNCTGA 15

RESULT 13
BM394638

LOCUS 18 bp mRNA linear EST 17-JAN-2002
DEFINITION 50072-2-5-B10.r.1 Chilcoat/Turkewitz cDNA (large fraction)
ACCESSION Tetrahymena thermophila cDNA, mRNA sequence.
BM394638
VERSION BM394638.1 GI:18194691
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 18)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
JOURNAL Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
SOURCE Location/Qualifiers
1..18 /organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1lb="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK-; Details on library preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 3 a 3 c 10 g 2 t
ORIGIN

Query Match 42.2% Score 7.6; DB 13; Length 18;
Best Local Similarity 57.1%; Pred. No. 6e+06;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 AUGGCCUAGCGUG 15
1:1 1:1 1:1 1:1
Db 2 ATGGGACAGCGCGT 15

RESULT 14
AA885697

LOCUS AA885697 19 bp mRNA linear EST 09-JUN-1998
DEFINITION OJ34f01.s1 NCI-CGAP Lu5 Homo sapiens cDNA clone IMAGE:1500217 3',
similar to TR:Q92842 Q92842 HOMOLOG OF YEAST UPF1. [1] ;, mRNA
sequence.

ACCESSION AA885697
VERSION AA885697.1 GI:3000805
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/cgicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.1nl.gov/bdrp/image/image.html
Insert Length: 691 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
SOURCE Location/Qualifiers
1..19 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="IMAGE:1500217"
/clone_1lb="NCI-CGAP Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 5 a 4 c 6 g 4 t
ORIGIN

Query Match 42.2% Score 7.6; DB 9; Length 19;
Best Local Similarity 57.1%; Pred. No. 6e+06;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 AAUGGCCUAGCGU 14
1:1 1:1 1:1 1:1
Db 1 AATAGCCAGCGCGT 14

RESULT 15
A1625518

LOCUS A1625518 19 bp mRNA linear EST 22-APR-1999
DEFINITION U55606.x1 NCI-CGAP-Ut2 Homo sapiens cDNA clone IMAGE:2283083 3',
similar to TR:P93237 P93237 PROLINE-RICH PROTEIN PRP2 PRECURSOR,
; contains MSRL.tl MSRL repetitive element ;, mRNA sequence.

ACCESSION A1625518

VERSION A1625518.1 GI:4650449

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 19)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

1. 19

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2283083"

/clone_lib="NCI-CGAP_Ut2"

/tissue_type="moderately-differentiated endometrial

adenocarcinoma, 3 pooled tumors"

/lab_host="DH10B"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Salt;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.85 Kb. Life Technologies catalog #:

11539-012"

BASE COUNT

7 a 11 c 1 g 0 t

ORIGIN

Query Match 42.2%; Score 7.6; DB 9; Length 19;
Best Local Similarity 50.0%; Pred. No. 6e+06;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4' GGGCUAUCGUGCG 17

11 : : 11:111

Db 19 GGGTTTGTGTCG 6

Search completed: May 22, 2003, 20:17:07.
Job time : 1317.82 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 18:55:07 ; Search time 38.7273 seconds
(without alignments)
142.540 Million cell updates/sec

Title: US-09-780-929-98

Perfect score: 18

Sequence: 1 aaugcccaucgugcgca 18

Scoring table: IDENTITY NUC

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 247290

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA:*

- 1: /cgn2-6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2-6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2-6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2-6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2-6/ptodata/1/ina/PTCUS.COMB.seq:*
- 6: /cgn2-6/ptodata/1/ina/backfilest.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11.4	63.3	17	US-08-292-620A-1886	Sequence 1886, Ap
2	11.4	63.3	17	US-08-292-620A-1977	Sequence 1977, Ap
3	11.4	63.3	17	US-09-071-845-1886	Sequence 1886, Ap
4	11.4	63.3	17	US-09-071-845-1977	Sequence 1977, Ap
5	10.6	58.9	20	US-08-418-071-6	Sequence 6, Appl
6	10.4	57.8	15	US-08-182-968A-497	Sequence 497, App
7	10.4	57.8	15	US-08-774-306A-497	Sequence 497, App
8	10.4	57.8	15	US-09-064-156A-497	Sequence 497, App
9	10.2	56.7	17	US-09-059-779-5	Sequence 5, Appl
10	10.2	56.7	17	US-08-584-040-5815	Sequence 5815, Ap
11	10.2	56.7	17	US-08-584-040-5816	Sequence 5816, Ap
12	10.2	56.7	17	US-08-584-040-5817	Sequence 5817, Ap
13	10.2	56.7	18	US-09-108-837-3	Sequence 3, Appl
14	10	55.6	12	US-08-948-097-7	Sequence 7, Appl
15	10	55.6	20	US-08-222-177A-108	Sequence 108, App
16	9.8	54.4	16	US-08-872-917-11	Sequence 11, Appl
17	9.8	54.4	17	US-08-584-040-5814	Sequence 5814, Ap
18	9.8	54.4	20	US-08-837-201C-66	Sequence 66, Appl
19	9.8	54.4	20	US-09-364-416-66	Sequence 66, Appl
20	9.6	53.3	17	US-08-584-040-7863	Sequence 7863, Ap
21	9.6	53.3	17	US-08-679-645-264	Sequence 264, App
22	9.6	53.3	18	US-09-143-212-60	Sequence 60, Appl
23	9.6	53.3	18	US-08-679-645-643	Sequence 643, App
24	9.6	53.3	19	US-07-794-400-16	Sequence 16, Appl
25	9.6	53.3	19	US-08-397-470-16	Sequence 16, Appl
26	9.6	53.3	20	US-08-356-405-11	Sequence 11, Appl
27	9.6	53.3	20	US-08-478-178A-66	Sequence 66, Appl

ALIGNMENTS

C 28	9.6	53.3	20	2	US-08-488-177-66	Sequence 66, Appl
C 29	9.6	53.3	20	2	US-08-481-072A-66	Sequence 66, Appl
C 30	9.6	53.3	20	2	US-08-664-336-66	Sequence 66, Appl
C 31	9.6	53.3	20	2	US-08-481-066A-66	Sequence 66, Appl
C 32	9.6	53.3	20	4	US-09-313-930-6	Sequence 6, Appl
C 33	9.6	53.3	20	4	US-08-943-731-546	Sequence 546, App
C 34	9.6	53.3	20	4	US-09-593-589-72	Sequence 72, Appl
C 35	9.6	53.3	20	4	US-08-829-637A-66	Sequence 66, Appl
C 36	9.4	52.2	12	4	US-09-281-418-54	Sequence 54, Appl
C 37	9.4	52.2	18	1	US-08-126-564A-30	Sequence 30, Appl
C 38	9.4	52.2	18	2	US-08-465-380-100	Sequence 100, App
C 39	9.4	52.2	18	2	US-08-480-478-13	Sequence 13, Appl
C 40	9.4	52.2	18	2	US-08-486-397-100	Sequence 100, App
C 41	9.4	52.2	18	2	US-08-486-399-100	Sequence 100, App
C 42	9.4	52.2	18	2	US-08-461-965-100	Sequence 100, App
C 43	9.4	52.2	18	2	US-08-326-110A-13	Sequence 13, Appl
C 44	9.4	52.2	18	2	US-08-634-641-100	Sequence 100, App
C 45	9.4	52.2	18	3	US-09-249-471-100	Sequence 100, App

RESULT 1
US-08-292-620A-1886

Sequence 1886, Application US/08292620A
Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,620A

FILING DATE: August 17, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895

FILING DATE: January 19, 1993

APPLICATION NUMBER: 07/989,849

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/149

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1886:

two

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1886

Query Match 63.3%; Score 11.4; DB 2; Length 17;
Best Local Similarity 92.3%; Pred. No. 7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCUACGGUGC 16
||||| |||||||
DB 2 GGCCUCGCGUGC 14

RESULT 2

US-08-292-620A-1977
Sequence 1977, Application US/08292620A
Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992

two

ATTORNEY/AGENT INFORMATION:

NAME: Waldbury, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1977:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1977

Query Match 63.3%; Score 11.4; DB 2; Length 17;
Best Local Similarity 92.3%; Pred. No. 7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCUACGGUGC 16
||||| |||||||
DB 2 GGCCUCGCGUGC 14

RESULT 3

US-09-071-845-1886
Sequence 1886, Application US/09071845
Patent No. 6132967

GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994

APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Waldbury, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1886:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1886

Query Match 63.3%; Score 11.4; DB 3; Length 17;
Best Local Similarity 92.3%; Pred. No. 7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCUACGGUGC 16
||||| |||||||
DB 2 GGCCUCGCGUGC 14


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RESULT 4
US-09-071-845-1977
; Sequence 1977, Application US/09071845
; Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Diaper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
City: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 1977:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1977

Query Match 63.3%; Score 11.4; DB 3; Length 17;
Best Local Similarity 92.3%; Pred. No. 7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGGCUAUGGUGC 16
DB 2 GGGCUGUGGUGC 14

RESULT 5
US-08-418-071-6
; Sequence 6, Application US/08418071
; Patent No. 5846705
GENERAL INFORMATION:
APPLICANT: Wu, Rey-Yuh
APPLICANT: You, Li-Ru
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF TWO CIRCULAR ssDNA
TITLE OF INVENTION: ASSOCIATED WITH BANANA BUNCHY TOP VIRUS AND METHOD FOR DETE
TITLE OF INVENTION: BANANA BUNCHY TOP VIRUS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
City: New York
STATE: New York
COUNTRY: United States
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,071
FILING DATE: 06-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: DCB-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc="Oligonucleotide primer BB-1"
ANTI-SENSE: YES
US-08-418-071-6

Query Match 58.9%; Score 10.6; DB 2; Length 20;
Best Local Similarity 58.8%; Pred. No. 2.1e+03;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 AUGCCUAGGUGCGA 18
DB 2 AUGGCTATCGAGCGAA 18

RESULT 6
US-08-182-968A-497/C
; Sequence 497, Application US/08182968A
; Patent No. 5610054
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
City: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
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SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,968A
FILING DATE: 13-JANUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,888
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-182-968A-497

Query Match          57.8%; Score 10.4; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches      8; Conservative      3; Mismatches      1; Indels      0; Gaps      0.

QY      2 AUGGCCUAUCCG 13
      1:||||:|:|
Db      14 ATGGCCTATTGG 3

RESULT 7
US-08-774-306A-497/C
Sequence 497, Application US/08774306A
Patent No. 5869253
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,306A
FILING DATE: December 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 497:

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 15
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-774-306A-497

Query Match
Best Local Similarity 57.8%; Score 10.4; DB 2; Length 15;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 AUGGCCUAVCGG 13
1:||||:|11
DB 14 ATGGCCTATTGG 3

RESULT 8
US-09-064-156A-497/c
: Sequence 497; Application US/09064156A
: Patent No. 6132966
: GENERAL INFORMATION:
: APPLICANT: Draper, Kenneth G.
: TITLE OF INVENTION: METHOD AND REAGENT FOR
: TITLE OF INVENTION: INHIBITING HEPATITIS C
: TITLE OF INVENTION: VIRUS REPLICATION
: NUMBER OF SEQUENCES: 498
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071-2066
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 MB
: MEDIUM TYPE: storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/064,156A
: FILING DATE: April 21, 1998
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/774,306
: FILING DATE: December 26, 1996
: APPLICATION NUMBER: 08/182,968
: FILING DATE: January 13, 1994
: APPLICATION NUMBER: 07/882,888
: FILING DATE: May 14, 1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Wardburg, Richard J.
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 234/083
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELE: 67-3510
: INFORMATION FOR SEQ ID NO: 497:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-09-064-156A-497

Query Match
Best Local Similarity 57.8%; Score 10.4; DB 3; Length 15;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 AUGGCCUAVCGG 13
1:||||:|11
DB 14 ATGGCCTATTGG 3

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RESULT 9
US-09-059-779-5
; Sequence 5, Application US/09059779
; Patent No. 6153743
; GENERAL INFORMATION:
; APPLICANT: Hubbell Earl A.
; APPLICANT: Lubert Stryer
; APPLICANT: Michael P. Miltmann
; TITLE OF INVENTION: Lithographic Mask Design and
; TITLE OF INVENTION: Synthesis of Diverse Probes on a Substrate
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rilter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: California
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/059,779
; FILING DATE: April 13, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rilter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: AFTYP015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-09-059-779-5
Query Match 56.7%; Score 10.2; DB 3; Length 15;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGGCCUAGCGGUC 16
Db 1 ATGGCAGATCATGC 15
RESULT 10
US-08-584-040-5815
; Sequence 5815, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5815:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-5815
Query Match 56.7%; Score 10.2; DB 4; Length 17;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 UGGCCUAGCGGUC 17
Db 3 UGGCCUAGCGGUC 17
RESULT 11
US-08-584-040-5816
; Sequence 5816, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040

FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5816:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-5816

Query Match 56.7%; Score 10.2; DB 4; Length 17;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 UGCGCUAUCGUGCG 17
||| || ||||| |
Db 2 UGUCUUCUGGUGUG 16

RESULT 12
US-08-584-040-5817
Sequence 5817, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5817:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-5817

Query Match 56.7%; Score 10.2; DB 4; Length 17;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 UGCGCUAUCGUGCG 17
||| || ||||| |
Db 1 UGUCUUCUGGUGUG 15

RESULT 13
US-09-108-837-3
Sequence 3, Application US/09108837
Patent No. 5972617
GENERAL INFORMATION:
APPLICANT: SAMI, Manabu
TITLE OF INVENTION: OLIGONUCLEOTIDE FOR DETECTING LACTIC ACID BACTERIA AND
FILE REFERENCE: SAMI
CURRENT APPLICATION NUMBER: US/09/108,837
CURRENT FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: 09-195268
EARLIER FILING DATE: 1997-07-07
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 18
TYPE: DNA
ORGANISM: Lactobacillus brevis
US-09-108-837-3

Query Match 56.7%; Score 10.2; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAUGCCUAUCGUG 15
||: ||| ||||: |
Db 1 AAUGCCAAATCGTG 15

RESULT 14
US-08-948-097-7
Sequence 7, Application US/08948097C
Patent No. 6103493
GENERAL INFORMATION:
APPLICANT: Skerra, Arne
APPLICANT: Voss, Selma
TITLE OF INVENTION: Streptavidin Mutelins
FILE REFERENCE: HDR 1119
CURRENT APPLICATION NUMBER: US/08/948,097C
CURRENT FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: DE 196 41 876.3
EARLIER FILING DATE: 1996-10-10
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 7
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: CDS
OTHER INFORMATION: Synthesized
US-08-948-097-7

Query Match 55.6%; Score 10; DB 3; Length 12;
Best Local Similarity 80.0%; Pred. No. 4.4e+03;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 AUGGUGCGA 18
1111111111

Db 1 ATGGGTGCGA 10

RESULT 15

US-08-222-177A-108/c
; Sequence 108, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dc-da)n.(dc-dt)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelstior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865, 601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd19p1
US-08-222-177A-108

Query Match 55.6%; Score 10; DB 1; Length 20;
Best Local Similarity 61.1%; Pred. No. 4.7e+03;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 A AUGGCUUUGCGUGCGA 18
111111111111111111

Db 18 AATGGCCAAAGGGTTAGA 1

Search completed: May 22, 2003, 20:18:25
Job time : 40.7273 secs

GenCore version 5.1.4-P5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 19:36:48 ; Search time 85.0909 Seconds

(without alignments)
279.329 Million cell updates/sec

Title: US-09-780-929-98

Perfect score: 18

Sequence: 1 aaugcccaucgugcgca 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 191488

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	10	US-09-780-929-98
2	11.2	62.2	17	9	US-09-780-533A-633
3	11.2	62.2	19	9	US-09-796-081-3
4	11.2	62.2	19	9	US-09-796-081-4
5	10.4	57.8	15	10	US-09-504-231A-519
6	10.4	57.8	15	10	US-09-274-553D-519
7	10.4	57.8	18	10	US-09-969-373-3464
8	10.4	57.8	20	9	US-10-068-160-36
9	10.2	56.7	17	9	US-09-780-533A-2300
10	10.2	56.7	17	9	US-09-780-533A-2662
11	10.2	56.7	18	10	US-09-969-373-2070
12	10	55.6	18	9	US-09-961-700A-29
13	10	55.6	20	9	US-09-232-785-373
14	9.8	54.4	17	9	US-09-825-805-737
15	9.6	53.3	17	9	US-09-825-805-712
16	9.6	53.3	17	9	US-09-961-077-264
17	9.6	53.3	17	9	US-09-848-754A-1942
18	9.6	53.3	17	9	US-09-848-754A-3017
19	9.6	53.3	18	9	US-09-961-077-643

ALIGNMENTS

20	9.6	53.3	18	9	US-10-132-652-18	Sequence 18, Appl
21	9.6	53.3	20	10	US-09-766-399-17	Sequence 17, Appl
22	9.4	52.2	17	9	US-09-877-478-300	Sequence 300, App
23	9.4	52.2	17	9	US-09-877-478-988	Sequence 988, App
24	9.4	52.2	17	9	US-09-877-478-989	Sequence 989, App
25	9.4	52.2	17	9	US-09-877-478-1719	Sequence 1719, App
26	9.4	52.2	17	9	US-09-877-478-1967	Sequence 1967, App
27	9.4	52.2	17	9	US-09-877-478-2309	Sequence 2309, App
28	9.4	52.2	18	10	US-09-969-373-2727	Sequence 2727, App
29	9.4	52.2	18	10	US-09-969-373-2729	Sequence 2729, App
30	9.4	52.2	18	10	US-09-969-373-3465	Sequence 3465, App
31	9.4	52.2	18	10	US-09-969-373-4573	Sequence 4573, App
32	9.4	52.2	19	9	US-10-080-959A-3	Sequence 3, Appl1
33	9.4	52.2	20	9	US-09-924-981-5	Sequence 5, Appl1
34	9.4	52.2	20	9	US-10-267-117-12	Sequence 135, Appl
35	9.2	51.1	15	10	US-09-504-231A-135	Sequence 135, App
36	9.2	51.1	15	10	US-09-274-553B-135	Sequence 135, App
37	9.2	51.1	17	9	US-09-780-533A-2301	Sequence 2301, App
38	9.2	51.1	17	9	US-09-780-533A-2661	Sequence 2661, App
39	9.2	51.1	17	9	US-09-848-754A-620	Sequence 620, App
40	9.2	51.1	17	10	US-09-866-108-9650	Sequence 9650, App
41	9.2	51.1	17	10	US-09-866-108-9651	Sequence 9651, App
42	9.2	51.1	17	10	US-09-866-108-9652	Sequence 9652, App
43	9.2	51.1	17	10	US-09-866-108-9653	Sequence 9653, App
44	9.2	51.1	18	9	US-09-961-700A-21	Sequence 21, Appl
45	9.2	51.1	18	9	US-09-747-377-211	Sequence 211, App

RESULT 1
US-09-780-929-98
Sequence 98, Application US/09780929
Patent No. US20020151693A1
GENERAL INFORMATION: Breaker, Ronald
APPLICANT: Breaker, Ronald
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: M88B00-884-H (500/001)
CURRENT APPLICATION NUMBER: US/09/780,929
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: US 60/181,360
PRIORITY FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PatentIn version 3.0
SEQ ID NO 98
LENGTH: 18
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 AAUGCCCAUCGUGCGCA 18
US-09-780-533A-633/C
Sequence 633, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Chowitra, Bharat

```

; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NCO Gene
; FILE REFERENCE: MBHR00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 633
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-633

Query Match
Best Local Similarity 62.2%; Score 11.2; DB 9; Length 17;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAUGGCCUAUCGUGC 16
DB 16 AATGATCTATCTGTGC 1

RESULT 3
US-09-796-081-3
; Sequence 3, Application US/09796081
; Publication No. US20030045538A1
; GENERAL INFORMATION:
; APPLICANT: Danaboyina, Ramalsh
; APPLICANT: Nadukkudy, Varghese E.
; APPLICANT: Joshy, Joseph
; TITLE OF INVENTION: VILOGEN LINKED ACRIDINE BASED MOLECULE AND PROCESS FOR
; FILE REFERENCE: 3108/01342
; CURRENT APPLICATION NUMBER: US/09/796,081
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-796-081-3

Query Match
Best Local Similarity 62.2%; Score 11.2; DB 9; Length 19;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAUGGCCUAUCGUGC 16
DB 2 ACTGCGCTTTCGCTGC 17

RESULT 4
US-09-796-081-4/c
; Sequence 4, Application US/09796081
; Publication No. US20030045538A1
; GENERAL INFORMATION:
; APPLICANT: Danaboyina, Ramalsh
; APPLICANT: Nadukkudy, Varghese E.
; APPLICANT: Joshy, Joseph
; TITLE OF INVENTION: VILOGEN LINKED ACRIDINE BASED MOLECULE AND PROCESS FOR
; FILE REFERENCE: 3108/01342
; CURRENT APPLICATION NUMBER: US/09/796,081
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 19
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-796-081-4

Query Match
Best Local Similarity 62.2%; Score 11.2; DB 9; Length 19;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAUGGCCUAUCGUGC 16
DB 18 ACTGCGCTTTCGCTGC 3

RESULT 5
US-09-504-231A-519/c
; Sequence 519, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: MGSWiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL
; FILE REFERENCE: tpi 247/282
; CURRENT FILING DATE: 2000-02-15
; CURRENT APPLICATION NUMBER: US/09/504,231A
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 519
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-519

Query Match
Best Local Similarity 57.8%; Score 10.4; DB 10; Length 15;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AUGGCCUAUCG 13
DB 14 AATGCGCTATTGC 3

RESULT 6
US-09-274-553D-519/c
; Sequence 519, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: MGSWiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS REL
; FILE REFERENCE: tpi 247/282
; CURRENT FILING DATE: 1999-03-23
; CURRENT APPLICATION NUMBER: US/09/274,553D
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
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PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3148
SOFTWARE: PatentIn version 3.0
SEQ ID NO 519
LENGTH: 15
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-519

Query Match 57.8%; Score 10.4; DB 10; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AUGGCCUAGCG 13
Db 14 ATGCCCTATTGG 3

RESULT 7
US-09-969-373-3464/c
Sequence 3464, Application US/09969373
Patent No. US20020133852A1
GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-07
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 3464
LENGTH: 18
TYPE: DNA
ORGANISM: Glycine max
US-09-969-373-3464

Query Match 57.8%; Score 10.4; DB 10; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 CUADCGUGGCA 18
Db 12 CTATCGTGGCA 1

RESULT 8
US-10-068-160-36/c
Sequence 36, Application US/10068160
Publication No. US20030060440A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLIMMAN, Dennis
APPLICANT: ISHII, Ken
APPLICANT: VERHEIJT, Daniela
TITLE OF INVENTION: OLIGODEXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/068,160
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 120
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-10-068-160-36

Query Match 57.8%; Score 10.4; DB 9; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCUAGCGUGC 16
Db 15 GCCTATCGATGC 4

RESULT 9
US-09-780-533A-2300/c
Sequence 2300, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Chowrira, Bharat
APPLICANT: Haeblerl, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBH800,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2300
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-2300

Query Match 56.7%; Score 10.2; DB 9; Length 17;
Best Local Similarity 53.3%; Pred. No. 2.2e+04;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGGCCUAGCGUGC 16
Db 17 ATGATCTATCTGTGC 3

RESULT 10
US-09-780-533A-2662/c
Sequence 2662, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
APPLICANT: Chowrira, Bharat
APPLICANT: Haeblerl, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBH800,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2662
LENGTH: 17
TYPE: RNA


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; ORGANISM: Homo sapiens
US-09-780-533A-2662

Query Match
Best Local Similarity 56.7%; Score 10.2; DB 9; Length 17;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAUGGCCUAGCGUG 15
DB 15 AATGATCTATCTGTG 1

RESULT 11
US-09-969-373-2070
; Sequence 2070, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Eiertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2070
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2070

Query Match
Best Local Similarity 56.7%; Score 10.2; DB 10; Length 18;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAUGGCCUAGCGUG 15
DB 4 AATGCCAATTGCTG 18

RESULT 12
US-09-961-700A-29
; Sequence 29, Application US/09961700A
; Publication No. US20020187482A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Zicai
; APPLICANT: Wang, Hong-Yan
; APPLICANT: Wallestedt, Claes
; TITLE OF INVENTION: Methods and Means of RNA Analysis
; FILE REFERENCE: 13522-003001
; CURRENT APPLICATION NUMBER: US/09/961,700A
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 60/235,029
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotide
US-09-961-700A-29

Query Match
Best Local Similarity 55.6%; Score 10; DB 9; Length 18;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
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OY 1 AAUGGCCUAGCGUGCGA 18
DB 1 AATGGGCTTCTGCTGCA 18

RESULT 13
US-09-232-785-373/C
; Sequence 373, Application US/09232785
; Publication No. US20030049612A1
; GENERAL INFORMATION:
; APPLICANT: International Paper Co.
; APPLICANT: Echt, Craig. S
; APPLICANT: Nelson, C. Dana
; TITLE OF INVENTION: MICROSATELLITE DNA MARKERS AND USES
; FILE REFERENCE: 4481/1E18US1
; CURRENT APPLICATION NUMBER: US/09/232,785
; CURRENT FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 09/232,884
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Pinus taeda L.
US-09-232-785-373

Query Match
Best Local Similarity 55.6%; Score 10; DB 9; Length 20;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 AAUGGCCUAGCGUGCGA 18
DB 18 AATGGCTATCGGACCA 1

RESULT 14
US-09-825-805-737
; Sequence 737, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Beaudry, Leo
; APPLICANT: Karpelsky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Svedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucle
; FILE REFERENCE: MBH800-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 737
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
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Title: US-09-780-929-98

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2	12.2	67.8	20	31	US-09-827-383-650	Sequence 650, App	
3	12.2	67.8	20	31	US-09-827-383-803	Sequence 803, App	
4	12.2	67.8	20	31	US-09-827-383-650	Sequence 650, App	
5	12.2	67.8	20	31	US-09-827-383A-803	Sequence 803, App	
6	11.8	65.6	16	1	PCT-US02-25943-8274	Sequence 8274, Ap	
7	11.8	65.6	16	1	PCT-US02-25943-18265	Sequence 18265, A	
8	11.8	65.6	16	42	US-10-227-565-8274	Sequence 8274, Ap	
9	11.8	65.6	16	42	US-10-227-565-18265	Sequence 18265, A	
10	11.8	65.6	20	15	US-09-198-452A-3336	Sequence 3336, Ap	
11	11.4	63.3	20	28	US-09-703-708-17627	Sequence 17627, A	
12	11.4	63.3	20	62	US-60-164-320-17627	Sequence 17627, A	
13	11.4	63.3	20	62	US-60-183-791-17627	Sequence 17627, A	
14	11.2	62.2	17	21	US-09-546-745A-1992	Sequence 1992, A	
15	11.2	62.2	19	30	US-09-780-533A-633	Sequence 633, App	
16	11.2	62.2	19	30	US-09-796-081-4	Sequence 81, Appl	
17	11.2	62.2	20	43	US-10-262-666-77	Sequence 77, Appl	
18	11.2	62.2	15	1	PCT-US02-25940-16232	Sequence 16232, A	
19	10.8	60.0	15	1	PCT-US02-25940-19783	Sequence 19783, A	
20	10.8	60.0	15	1	PCT-US02-25942-1512	Sequence 1512, Ap	
21	10.8	60.0	15	1	PCT-US02-25942-1512	Sequence 1512, Ap	

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22 10.8 60.0 15 1 PCT-US02-25942-1775 Sequence 1775, Ap
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24 10.8 60.0 15 17 US-10-227-563-16232 Sequence 16232, A
25 10.8 60.0 15 42 US-10-227-563-19783 Sequence 19783, A
26 10.8 60.0 15 42 US-10-227-567-1512 Sequence 1512, A
27 10.8 60.0 15 42 US-10-227-567-1775 Sequence 1775, Ap
28 10.8 60.0 20 7 US-08-341-469-10 Sequence 10, Appl
29 10.6 58.9 20 8 US-08-484-735-6 Sequence 6, Appl
30 10.6 58.9 20 19 US-09-514-000-11863 Sequence 11863, A
31 10.4 57.8 15 1 PCT-US01-05126-16 Sequence 16, Appl
32 10.4 57.8 15 11 US-08-774-306-497 Sequence 497, App
33 10.4 57.8 15 11 US-09-274-553-1054 Sequence 1054, App
34 10.4 57.8 15 16 US-09-274-553B-519 Sequence 519, App
35 10.4 57.8 15 16 US-09-274-553C-519 Sequence 519, App
36 10.4 57.8 15 16 US-09-274-553D-519 Sequence 519, App
37 10.4 57.8 15 19 US-09-504-231A-519 Sequence 519, App
38 10.4 57.8 15 19 US-09-504-231B-519 Sequence 519, App
39 10.4 57.8 15 23 US-09-611-931-519 Sequence 519, App
40 10.4 57.8 15 24 US-09-611-931A-519 Sequence 519, App
41 10.4 57.8 15 24 US-09-633-515-497 Sequence 497, App
42 10.4 57.8 16 28 US-09-705-400-26 Sequence 26, Appl
43 10.4 57.8 16 28 US-09-705-400-61 Sequence 61, Appl
44 10.4 57.8 16 30 US-09-765-400-26 Sequence 26, Appl
45 10.4 57.8 16 30 US-09-765-400-61 Sequence 61, Appl
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ALIGNMENTS

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RESULT 1
US-09-780-929-98
; Sequence 98, Application US/09780929
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc
; APPLICANT: Breaker, Ronald
; APPLICANT: Belgelman, Leo
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH800-884-H (500/001)
; CURRENT APPLICATION NUMBER: US/09/780, 929
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US 60/181,360
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 'Enzymatic Nucleic Acid
US-09-780-929-98

Query Match 100.0%; Score 18; DB 30; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAUGGCCUUAUCGGUGCGA 18
Db 1 AAUGGCCUUAUCGGUGCGA 18

RESULT 2
US-09-827-383-650/c
; Sequence 650, Application US/09827383
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Macdonald Morris
; APPLICANT: Tom Ryder
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Tag Nucleic Acids and Probe Arrays
; FILE REFERENCE: 3108
; CURRENT APPLICATION NUMBER: US/09/827,383
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; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/195,585
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 650
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-383-650

Query Match 67.8%; Score 12.2; DB 31; Length 20;
Best Local Similarity 64.7%; Pred. No. 2e+04;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAUGGCCUUAUCGGUGCG 17
Db 19 AATCGCTCTCGAGCG 3

RESULT 3
US-09-827-383-803
; Sequence 803, Application US/09827383
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Macdonald Morris
; APPLICANT: Tom Ryder
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Tag Nucleic Acids and Probe Arrays
; FILE REFERENCE: 3108
; CURRENT APPLICATION NUMBER: US/09/827,383
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/195,585
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 803
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-383-803

Query Match 67.8%; Score 12.2; DB 31; Length 20;
Best Local Similarity 64.7%; Pred. No. 2e+04;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 AUGGCCUUAUCGGUGCGA 18
Db 4 ATGCACATCGTTGGCA 20

RESULT 4
US-09-827-383A-650/c
; Sequence 650, Application US/09827383A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Macdonald Morris
; APPLICANT: Tom Ryder
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Tag Nucleic Acids and Probe Arrays
; FILE REFERENCE: 3108
; CURRENT APPLICATION NUMBER: US/09/827,383A
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/195,585
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 650
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
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( ; LOCATION: (1820695)...(1820710)
; OTHER INFORMATION: Chromosome - 1 Strand = positive ConnectionObjectNumber = 19657
US-10-227-565-18265

Query Match
Best Local Similarity 65.6%; Score 11.8; DB 42; Length 16;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGCCUACGCGCGA 18
    |||||:|:|:|
Db 2 GGCTATCGCGCGA 16

RESULT 10
US-09-198-452A-3336/C
; Sequence 3336, Application US/09198452A
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3336
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-3336

Query Match
Best Local Similarity 65.6%; Score 11.8; DB 15; Length 20;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAUGCCUACGCGUG 15
    |||||:|:|:|
Db 20 AATGCTATCGATG 6

RESULT 11
US-09-703-708-17627
; Sequence 17627, Application US/09703708
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15804)C
; CURRENT APPLICATION NUMBER: US/09/703,708
; CURRENT FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/164,320
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/183,791
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 17627
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-09-703-708-17627

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 28; Length 20;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGCGCUACGCGUG 15
    :|||:|:|:|
Db 2 TGGCTATCTGTG 14

RESULT 12
US-60-164-320-17627
; Sequence 17627, Application US/60164320

GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15804)A
; CURRENT APPLICATION NUMBER: US/60/164,320
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 17627
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-164-320-17627

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 60; Length 20;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGCGCUACGCGUG 15
    :|||:|:|:|
Db 2 TGGCTATCTGTG 14

RESULT 13
US-60-183-791-17627
; Sequence 17627, Application US/60183791
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15804)B
; CURRENT APPLICATION NUMBER: US/60/183,791
; CURRENT FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 17627
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-183-791-17627

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 62; Length 20;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGCGCUACGCGUG 15
    :|||:|:|:|
Db 2 TGGCTATCTGTG 14

RESULT 14
US-09-546-745A-1992/C
; Sequence 1992, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1992
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-1992

Query Match
Best Local Similarity 62.2%; Score 11.2; DB 21; Length 17;
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Best Local Similarity 62.5%; Pred. No. 7.8e+04;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 UGCGCUAUCGUGCGA 18
:|||||:|||||
Db 16 TGCGCCATAGTGTCCA 1

RESULT 15

US-09-780-533A-633/C
; Sequence 633, Application US/09780533A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowdhra, Bharat
; APPLICANT: Haebell, Pete
; TITLE OF INVENTION: Method and Reagent for the inhibition of NOGO Gene
; FILE REFERENCE: MBH00, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 633
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-633

Query Match 62.2%; Score 11.2; DB 30; Length 17;
Best Local Similarity 56.2%; Pred. No. 7.8e+04;

Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAUGCCUAUCGUGCG 16
|||:|:|:|:|:|
Db 16 AATGATCTATCTGTGC 1

Search completed: May 22, 2003, 21:22:05
Job time : 2076.36 secs

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 19:04:38 ; Search time 445.636 Seconds

(without alignments)
209.509 Million cell updates/sec

Title: US-09-780-929-98

Perfect score: 18

Sequence: 1 aaugccuauugcgugcg 18

Scoring table: IDENTITY_NUC
Gapox 10.0, Gapext 1.0

Searched: 6438716 seqs, 2593467500 residues

Total number of hits satisfying chosen parameters: 667140

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Pending Patents.NA.New.*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq.*
8: /cgn2_6/ptodata/2/pna/US12_NEW_COMB.seq.*
9: /cgn2_6/ptodata/2/pna/US13_NEW_COMB.seq.*
10: /cgn2_6/ptodata/2/pna/US14_NEW_COMB.seq.*
11: /cgn2_6/ptodata/2/pna/US15_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11.8	65.6	19	1	PCT-US03-04088-255
2	11.8	65.6	20	6	US-09-827-383B-1775
3	11.8	65.6	20	8	US-10-289-762-3336
4	11.4	63.3	18	9	US-10-259-273-36
5	10.8	60.0	15	8	US-10-367-892-16232
6	10.8	60.0	15	8	US-10-367-892-19783
7	10.8	60.0	15	8	US-10-303-778-1079
8	10.8	60.0	15	8	US-10-287-787-23056
9	10.8	60.0	16	8	US-10-287-787-23057
10	10.8	60.0	17	1	PCT-US03-10154-33
11	10.8	60.0	17	8	US-10-404-724-33
12	10.8	60.0	18	8	US-10-237-016A-39
13	10.8	60.0	18	9	US-10-217-106-47
14	10.8	60.0	18	9	US-10-237-016-39
15	10.8	60.0	19	8	US-10-287-787-16018
16	10.8	60.0	19	8	US-10-287-787-22109
17	10.8	60.0	20	6	US-09-827-383B-232
18	10.6	58.9	18	9	US-10-168-424-43
19	10.4	57.8	15	6	US-09-274-553E-519
20	10.4	57.8	15	8	US-10-287-787-12676
21	10.4	57.8	16	8	US-10-287-787-142
22	10.4	57.8	16	8	US-10-287-787-6051

C 23	10.4	57.8	16	8	US-10-287-787-20529	Sequence 20529, A
C 24	10.4	57.8	16	8	US-10-287-787-26977	Sequence 26977, A
C 25	10.4	57.8	17	9	US-10-084-839-3310	Sequence 3310, Ap
C 26	10.4	57.8	18	8	US-10-299-054A-7571	Sequence 7571, Ap
C 27	10.4	57.8	18	8	US-10-299-054A-11547	Sequence 11547, A
C 28	10.4	57.8	19	9	US-10-259-275-73	Sequence 73, Appl
C 29	10.4	57.8	19	9	US-10-358-037-4	Sequence 4, Appl
C 30	10.4	57.8	20	1	PCT-US02-40955-22	Sequence 22, Appl
C 31	10.4	57.8	20	8	US-10-274-586-88	Sequence 88, Appl
C 32	10.2	56.7	15	8	US-10-367-892-12063	Sequence 12063, A
C 33	10.2	56.7	15	8	US-10-367-892-12851	Sequence 12851, A
C 34	10.2	56.7	15	8	US-10-367-892-14893	Sequence 14893, A
C 35	10.2	56.7	15	8	US-10-367-892-12461	Sequence 12461, A
C 36	10.2	56.7	15	8	US-10-287-787-1285	Sequence 1285, Ap
C 37	10.2	56.7	15	8	US-10-287-787-1488	Sequence 1488, Ap
C 38	10.2	56.7	15	8	US-10-287-787-6615	Sequence 6615, Ap
C 39	10.2	56.7	15	8	US-10-287-787-6616	Sequence 6616, Ap
C 40	10.2	56.7	15	8	US-10-287-787-19392	Sequence 19392, A
C 41	10.2	56.7	15	8	US-10-287-787-19393	Sequence 19393, A
C 42	10.2	56.7	16	8	US-10-367-892-6101	Sequence 6101, Ap
C 43	10.2	56.7	16	8	US-10-367-892-6102	Sequence 6102, Ap
C 44	10.2	56.7	16	8	US-10-299-054A-4121	Sequence 4121, Ap
C 45	10.2	56.7	16	8	US-10-299-054A-5693	Sequence 5693, Ap

ALIGNMENTS

RESULT 1
PCT-US03-04088-255
Sequence 255, Application PCT/US0304088
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Mcswigen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 255
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/sRNA sens
OTHER INFORMATION: region
PCT-US03-04088-255

Query Match 65.6%, Score 11.8; DB 1; Length 19;
Best Local Similarity 86.7%, Pred. No. 8.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
3 UGCGCUAUGGUGCG 17
||||| ||| |||||

Db 5 UGCGCAUCCGUGCG 19

RESULT 2

US-09-827-383B-1775/c
; Sequence 1775, Application US/09827383B
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; APPLICANT: Morris, Macdonald
; APPLICANT: Ryder, Thomas
; APPLICANT: Lockhart, David
; APPLICANT: Altimetrix, Inc.
; TITLE OF INVENTION: Tag Nucleic Acids and Probe Arrays
; FILE REFERENCE: 3108.1
; CURRENT APPLICATION NUMBER: US/09/827,383B
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/195,585
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 1775
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-827-383B-1775

Query Match 65.6%; Score 11.8; DB 6; Length 20;
Best Local Similarity 73.3%; Pred. No. 8.1e+03;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAUGCCUAUGGUG 15

Db 19 AAGCGCTATGCGG 5

RESULT 3

US-10-289-762-3336/c
; Sequence 3336, Application US/10289762
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3336
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-3336

Query Match 65.6%; Score 11.8; DB 8; Length 20;
Best Local Similarity 66.7%; Pred. No. 8.1e+03;

Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAUGCCUAUGGUG 15

Db 20 AATGGCTATGCGG 6

RESULT 4

US-10-259-275-56
; Sequence 56, Application US/10259275
; GENERAL INFORMATION:
; APPLICANT: Lemon, Stanley M.
; APPLICANT: Yi, Minkyung
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
; FILE REFERENCE: 265.0007 0120
; CURRENT APPLICATION NUMBER: US/10/259,275

; CURRENT FILING DATE: 2003-01-13

; PRIOR APPLICATION NUMBER: US 60/171,909

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: US 09/747,419

; PRIOR FILING DATE: 2000-12-23

; PRIOR APPLICATION NUMBER: US 60/325,236

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US 60/338,123

; PRIOR FILING DATE: 2001-11-13

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 56

; LENGTH: 18

; TYPE: DNA

; ORGANISM: ARTIFICIAL

; FEATURE: OTHER INFORMATION: primer

US-10-259-275-56

Query Match 63.3%; Score 11.4; DB 9; Length 18;

Best Local Similarity 69.2%; Pred. No. 1.4e+04;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAUGCCUAUGGUG 13

Db 5 AATGGCTATGCG 17

RESULT 5

US-10-367-892-16232
; Sequence 16232, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans RI complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices -703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 16232
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans RI complete genome, Plasmid
; FEATURE:
; LOCATION: (1951714)...(1951728)
; OTHER INFORMATION: Chromosome - 1 Strand - positive ConnectonObjectNumber = 18
US-10-367-892-16232

Query Match 60.0%; Score 10.8; DB 8; Length 15;

Best Local Similarity 71.4%; Pred. No. 2.9e+04;

Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCUAUGGUGCG 17

Db 2 GGCCGTCGTCGCG 15

RESULT 6

US-10-367-892-19783
; Sequence 19783, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans RI complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices -703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 19783
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans RI complete genome, Plasmid
; FEATURE:

```

; LOCATION: (2409107)...(2409121)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectorObjectNumber = 23195
US-10-367-892-19783
Query Match
Best Local Similarity 60.0%; Score 10.8; DB 8; Length 15;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCUAGCGGCG 17
    ||| :|||:|
DB 2 GGCGGTGCGTGGC 15

RESULT 7
US-10-303-778-1079
; Sequence 1079, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1079
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-1079
Query Match
Best Local Similarity 60.0%; Score 10.8; DB 9; Length 15;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCUAGCGGCG 17
    |||:|:|:|
DB 2 GGCGTATGCGTGG 15

RESULT 8
US-10-287-787-23056
; Sequence 23056, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 23056
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (3325540)...(3325555)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectorObjectNumber = 25456
US-10-287-787-23056
Query Match
Best Local Similarity 60.0%; Score 10.8; DB 8; Length 16;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 UGGCCUAGCGGCG 16
    :|||:|:|:|
DB 2 TCGCCTATCGGCGC 15

RESULT 9
US-10-287-787-23057/C
; Sequence 23057, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 23057
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (3325540)...(3325555)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectorObjectNumber = 25
US-10-287-787-23057
Query Match
Best Local Similarity 60.0%; Score 10.8; DB 8; Length 16;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 UGGCCUAGCGGCG 16
    :|||:|:|:|
DB 15 TCGCCTATCGGCGC 2

RESULT 10
PCT-US03-10154-33/C
; Sequence 33, Application PC/TUS0310154
; GENERAL INFORMATION:
; APPLICANT: XOMA TECHNOLOGY LTD.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; FILE REFERENCE: 13698MO01
; CURRENT APPLICATION NUMBER: PCT/US03/10154
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homosapiens
; NAME/KEY: misc.feature
; FEATURE:
; OTHER INFORMATION: ING-1 Heavy Chain Oligos Low Risk Primers -Reverse Primer GR
; NAME/KEY: misc.feature
; OTHER INFORMATION: ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR
PCT-US03-10154-33
Query Match
Best Local Similarity 60.0%; Score 10.8; DB 1; Length 17;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAUGGCCUAGCGU 14
    ||||| :|||:|
DB 15 AAGGCCATCGGT 2

RESULT 11
US-10-404-724-33/C
; Sequence 33, Application US/10404724
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; FILE REFERENCE: 13698US01
; CURRENT APPLICATION NUMBER: US/10/404,724
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
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; SOFTWARE: Patentin version 3.2
; SEQ ID NO 33
; LENGTH: 17
; TYPE: DNA
; ORGANISM: HomoSapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: ING-1 Heavy Chain Oligos Low Risk Primers -Reverse Primer GR
; NAME/KEY: misc.feature
; OTHER INFORMATION: ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR
US-10-404-724-33
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Query Match          60.0%; Score 10.8; DB 8; Length 17;
Best Local Similarity 71.4%; Pred. No. 3e+04;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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OY 1 AAGGCCUAGCGU 14
    |||||1:||||
Db 15 AAGGCCCATCGGT 2
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RESULT 12
US-10-237-016A-39/c
; Sequence 39, Application US/10237016A
; GENERAL INFORMATION:
; APPLICANT: OHTSUBO, KENICHI
; APPLICANT: OKADOME, HIROSHI
; APPLICANT: NAKAMURA, SUMIKO
; APPLICANT: HARAGUCHI, KAZUTOMO
; APPLICANT: YOZA, KOICHI
; APPLICANT: OKUNISHI, TOMOYA
; APPLICANT: SUZUKI, KEIICHI
; TITLE OF INVENTION: DNA-LEVEL RICE PALATABILITY EVALUATION METHOD, AND METHOD OF SELF
; TITLE OF INVENTION: PALATABLE RICE THROUGH ANALYSIS OF HALF GRAIN OF UNHULLED/UNPOLI
; FILE REFERENCE: 227527USOX
; CURRENT APPLICATION NUMBER: US/10/237,016A
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: JP 2001-273689
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-237-016A-39
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Query Match          60.0%; Score 10.8; DB 8; Length 18;
Best Local Similarity 57.1%; Pred. No. 3e+04;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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OY 1 AAGGCCUAGCGU 14
    |||||1:||||
Db 17 AATCGCATATCGGT 4
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```
RESULT 13
US-10-217-106-47/c
; Sequence 47, Application US/10217106
; GENERAL INFORMATION:
; APPLICANT: OHTSUBO, KENICHI
; APPLICANT: NAKAMURA, SUMIKO
; APPLICANT: MIYAMURA, TSUYOSHI
; APPLICANT: KUMO, SATOSHI
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: Method of detecting the presence or absence of mixed varieties in
; TITLE OF INVENTION: and identifying the mixed varieties in
; FILE REFERENCE: 226360USOX
; CURRENT APPLICATION NUMBER: US/10/217,106
; CURRENT FILING DATE: 2002-08-13
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; PRIOR APPLICATION NUMBER: JP 2001-250308
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 47
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-217-106-47
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```
Query Match          60.0%; Score 10.8; DB 9; Length 18;
Best Local Similarity 57.1%; Pred. No. 3e+04;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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```
OY 1 AAGGCCUAGCGU 14
    |||||1:||||
Db 17 AATCGCATATCGGT 4
```

```
RESULT 14
US-10-237-016-39/c
; Sequence 39, Application US/10237016
; GENERAL INFORMATION:
; APPLICANT: OHTSUBO, KENICHI
; APPLICANT: OKADOME, HIROSHI
; APPLICANT: NAKAMURA, SUMIKO
; APPLICANT: HARAGUCHI, KAZUTOMO
; APPLICANT: YOZA, KOICHI
; APPLICANT: OKUNISHI, TOMOYA
; APPLICANT: SUZUKI, KEIICHI
; TITLE OF INVENTION: DNA-LEVEL RICE PALATABILITY EVALUATION METHOD, AND METHOD OF S
; TITLE OF INVENTION: PALATABLE RICE THROUGH ANALYSIS OF HALF GRAIN OF UNHULLED/UNP
; FILE REFERENCE: 227527USOX
; CURRENT APPLICATION NUMBER: US/10/237,016
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: JP 2001-273689
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-237-016-39
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Query Match          60.0%; Score 10.8; DB 9; Length 18;
Best Local Similarity 57.1%; Pred. No. 3e+04;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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```
OY 1 AAGGCCUAGCGU 14
    |||||1:||||
Db 17 AATCGCATATCGGT 4
```

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RESULT 15
US-10-287-787-16018
; Sequence 16018, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 16018
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
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; FEATURE:
; LOCATION: (2427911)...(2427929)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectionObjectNumber = 17744
US-10-287-787-16018

Query Match      60.0%; Score 10.8; DB 8; Length 19;
Best Local Similarity 78.6%; Pred. No. 3e+04;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 5 GCCUACGCGGCGCA 18
   ||| :||| |||
Db 4 GCCCATCGCGCGCA 17

Search completed: May 22, 2003, 21:35:59
Job time : 448.636 secs
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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 18:59:38 ; Search time 1728.64 seconds

(without alignments)
218.170 Million cell updates/sec

Title: US-09-780-929-97

Perfect score: 15
Sequence: 1 agnaacgugaagau 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 1600790

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	15	100.0	15	US-09-780-929-97	Sequence 97, Appl
2	12	80.0	17	US-09-277-0268-1704	Sequence 1704, Ap
3	11.4	76.0	20	US-09-201-2284-3093	Sequence 3093, Ap
4	11.4	76.0	20	US-10-003-919-50	Sequence 50, Appl
5	11	73.3	19	US-60-216-745-13493	Sequence 13493, A
6	10.8	72.0	17	US-09-730-2898-606	Sequence 606, App
7	10.8	72.0	17	US-09-730-2898-607	Sequence 607, App
8	10.8	72.0	18	US-09-579-536-4	Sequence 4, Appl
9	10.8	72.0	18	US-09-579-536-4	Sequence 4, Appl
10	10.8	72.0	18	US-09-688-078-12	Sequence 12, Appl
11	10.8	72.0	18	US-10-213-329-4	Sequence 4, Appl
12	10.8	72.0	18	US-60-216-745-5964	Sequence 5964, Ap
13	10.8	72.0	20	PCR-US02-03159-22	Sequence 22, Appl
14	10.8	72.0	20	US-09-068-506-50	Sequence 50, Appl
15	10.8	72.0	20	US-09-514-000-12603	Sequence 12603, A
16	10.8	72.0	20	US-09-514-000-15028	Sequence 15028, A
17	10.8	72.0	20	US-09-703-708-12172	Sequence 12172, A
18	10.8	72.0	20	US-60-164-320-12172	Sequence 12172, A
19	10.8	72.0	20	US-60-183-791-12172	Sequence 12172, A
20	10.4	69.3	12	PCR-US98-26935-217	Sequence 217, App
21	10.4	69.3	12	US-09-215-436-217	Sequence 217, App

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22 10.4 69.3 12 22 US-09-581-970A-217 Sequence 217, App
23 10.4 69.3 17 21 US-09-546-745A-5653 Sequence 5653, Ap
24 10.4 69.3 17 30 US-09-792-818-40 Sequence 40, Appl
25 10.4 69.3 17 30 US-09-792-818-41 Sequence 41, Appl
26 10.4 69.3 17 30 US-09-792-818-222 Sequence 222, App
27 10.4 69.3 17 30 US-09-792-818-223 Sequence 223, App
28 10.4 69.3 17 30 US-09-792-818-562 Sequence 562, App
29 10.4 69.3 17 64 US-60-201-255-24 Sequence 24, Appl
30 10.4 69.3 19 36 US-09-969-373-2697 Sequence 2697, Ap
31 10.2 68.0 15 1 PCT-US02-25942-54 Sequence 54, Appl
32 10.2 68.0 15 1 PCT-US02-25942-55 Sequence 55, Appl
33 10.2 68.0 15 1 PCT-US02-25942-56 Sequence 56, Appl
34 10.2 68.0 15 1 PCT-US02-25942-57 Sequence 57, Appl
35 10.2 68.0 15 11 US-08-774-306-447 Sequence 447, App
36 10.2 68.0 15 16 US-09-274-553-1004 Sequence 1004, Ap
37 10.2 68.0 15 16 US-09-274-553B-469 Sequence 469, App
38 10.2 68.0 15 16 US-09-274-553C-469 Sequence 469, App
39 10.2 68.0 15 16 US-09-274-553D-469 Sequence 469, App
40 10.2 68.0 15 19 US-09-504-231A-469 Sequence 469, App
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42 10.2 68.0 15 23 US-09-611-931-469 Sequence 469, App
43 10.2 68.0 15 23 US-09-611-931A-469 Sequence 469, App
44 10.2 68.0 15 24 US-09-633-515-447 Sequence 447, App
45 10.2 68.0 15 42 US-10-227-567-54 Sequence 54, Appl
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ALIGNMENTS

RESULT 1
US-09-780-929-97

Sequence 97, Application US/09780929

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: Breaker, Ronald

TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity

FILE REFERENCE: MBH80-884-H (580/901) 929

CURRENT FILING DATE: US/09/780, 929

PRIOR APPLICATION NUMBER: 2001-02-08

PRIOR FILING DATE: 2000-02-08

NUMBER OF SEQ ID NOS: 126

SOFTWARE: Patent version 3.0

SEQ ID NO 97

LENGTH: 15

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-780-929-97

Query Match

Best Local Similarity 100.0%; Score 15; DB 30; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGUAAACGUGAAGAU 15

Db 1 AGUAAACGUGAAGAU 15

US-09-277-026B-1704

Sequence 1704, Application US/09277026B

GENERAL INFORMATION:

APPLICANT: Pavco, Pamela

APPLICANT: Roberts, Elisabeth

APPLICANT: Jarvis, Thale

APPLICANT: Coesholt, Claire

APPLICANT: MCSwigen, James

TITLE OF INVENTION: Method and Reagents for the Treatment of Diseases or Conditions R

FILE REFERENCE: MBH800-824-A (239/121)

CURRENT APPLICATION NUMBER: US/09/277, 026B
CURRENT FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/079, 678
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 6652
SOFTWARE: Patent version 3.0
SEQ ID NO 1704
LENGTH: 17
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: Oligonucleotide substrate
US-09-277-026B-1704

Query Match

Best Local Similarity 80.0%; Score 12; DB 16; Length 17;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGUAAACGUGA 12

Db 5 AGUAAACGUGA 16

RESULT 3
US-09-201-228A-3093

Sequence 3093, Application US/09201228A

GENERAL INFORMATION:

APPLICANT: Griffiths, Remy

APPLICANT: Holseth, Susan K.

APPLICANT: Zagursky, Robert John

APPLICANT: Metcalf, Benjamin J.

APPLICANT: Peek, Joel A.

APPLICANT: Sankaran, Banumathi

APPLICANT: Fletcher, Leah Diane

TITLE OF INVENTION: CHLAMYDIA TRACHOMATIS GENOMIC SEQUENCE AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF

TITLE OF INVENTION: INFECTION

FILE REFERENCE: 9710-0004-999

CURRENT APPLICATION NUMBER: US/09/201, 228A

CURRENT FILING DATE: 1998-11-30

PRIOR APPLICATION NUMBER: US 60/107, 077

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: FR 97-16034

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: FR 97-15041

PRIOR FILING DATE: 1997-11-28

NUMBER OF SEQ ID NOS: 5981

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3093

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Primer

US-09-201-228A-3093

Query Match

Best Local Similarity 76.0%; Score 11.4; DB 16; Length 20;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 AUAACGUGAAGAU 15

Db 2 ATAACGTGAGAT 14

US-10-003-919-50/C

Sequence 50, Application US/10003919

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

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Query Match Score 10.8; DB 22; Length 18;
Best Local Similarity 71.4%; Pred. No. 1e+05;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0
OY 2 GAUACGUGAGAU 15
    ||| |||||
Db 1 GAGACCGTGAAGAT 14

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Query Match	72.0%	Score 10.8;	DB 42;	Length 18;
Best Local Similarity	71.4%	Pred. No. 1e+05;		
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				Indels
				Gaps
QY	2 GAUACGCGTAGACU	15		
Db	1 GAGACCGTGAAGAT	14		

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RESULT 12
US-60-216-745-5964
Sequence 5964, Application US/60216745
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marla
APPLICANT: Chumakov, Ilya
APPLICANT: Abdurahim, Hadi
APPLICANT: Dufauré-Gare, Isabelle
TITLE OF INVENTION: BIOMOLETIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY
FILE REFERENCE: 84.051.PRO
CURRENT APPLICATION NUMBER: US/60/216, 745
CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ. ID NOS: 13665
SOFTWARE: Patent.pm
SEQ. ID NO 5964
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-25537 for SEQ. 1433,
US-60-216-745-5964

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; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
; FILE REFERENCE: RTS-0256
; CURRENT APPLICATION NUMBER: US/10/003,919
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-003-919-50

Query Match
Best Local Similarity 76.0%; Score 11.4; DB 38; Length 20;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GAUACGUGAAGA 14
Db 20 GACACGCGAAGA 8

RESULT 5
US-60-216-745-13493
; Sequence 13493, Application US/60216745
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Abderrahim, Hadi
; APPLICANT: Dufaire-Gare, Isabelle
; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY...
; FILE REFERENCE: 84, US1.PPO
; CURRENT APPLICATION NUMBER: US/60/216,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 13665
; SOFTWARE: Patent.pm
; SEQ ID NO 13493
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-50547 for SEQ 4431, in complen
US-60-216-745-13493

Query Match
Best Local Similarity 73.3%; Score 11; DB 65; Length 19;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UACGUGAAGA 14
Db 3 TAACGTGAGA 13

RESULT 6
US-09-730-289B-606/C
; Sequence 606, Application US/09730289B
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 606

; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-606

Query Match
Best Local Similarity 72.0%; Score 10.8; DB 29; Length 17;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAUACGUGAAGA 14
Db 17 AGATACATGAGA 4

RESULT 7
US-09-730-289B-607/C
; Sequence 607, Application US/09730289B
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 607
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-607

Query Match
Best Local Similarity 72.0%; Score 10.8; DB 29; Length 17;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGAUACGUGAAGA 14
Db 15 AGATATGTGAGA 2

RESULT 8
US-09-579-536-4
; Sequence 4, Application US/09579536
; GENERAL INFORMATION:
; APPLICANT: MACIAG, Thomas
; APPLICANT: ZIMRIN, Ann B.
; APPLICANT: SMALL, Deena J.
; APPLICANT: PRIDOVSKY, Igor A.
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS
; FILE REFERENCE: 36-102 (200036,0010) Maciag et al.
; CURRENT APPLICATION NUMBER: US/09/579,536
; CURRENT FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/199,865
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US97/09407
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/018,841
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PCR primer
US-09-579-536-4
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